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Run on: July 10, 2003, 12:30:15 ; Search time 21.5855 seconds
 (without alignments)
 2286.817 Million cell updates/sec

Title: US-09-813-718-10_COPY_48_471

Sequence: 1 MSYKAAGEDYKACCPPGNP.....VTDIEVKERFMTIRKLSFDFQ 424

Scoring table: BIOSUM62

Scoring table: Gapext 10.0 , Gapext 0.5

Searched: 445758 seqs, 118419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA,*

- 1: /cgn2_6/pctodata/2/pubpaa/US07_NEW_PUB.pep:*
- 2: /cgn2_6/pctodata/2/pubpaa/PCTN_NEW_PUB.pep:*
- 3: /cgn2_6/pctodata/2/pubpaa/US06_NEW_PUBCOMB.pep:*
- 4: /cgn2_6/pctodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/pctodata/2/pubpaa/PCTRIS_PUBCOMB.pep:*
- 6: /cgn2_6/pctodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/pctodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/pctodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/pctodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/pctodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/pctodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/pctodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/pctodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/pctodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
 RESULT 1
 US-09-813-718-12
 ; Sequence 12, Application US/09813-718
 ; Publication No. US2002010182666A1
 ; INTERNAL INFORMATION:
 ; APPLICANT: SCHIMMEL, Paul
 ; APPLICANT: Wakasugi, Kei, Buke
 ; TITLE OF INVENTION: Human Aminocycl-tRNA Synthetase Polypeptides Useful For
 ; TITLE OF INVENTION: The Regulation of Angiogenesis
 ; FILE REFERENCE: 00-221
 ; CURRENT APPLICATION NUMBER: US/09-813,718
 ; CURRENT FILING DATE: 2001-03-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 12
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: human mini
 ; OTHER INFORMATION: TPRs in PET20B

Query Match: 100.0%; Score: 2246; DB: 9; Length: 437;

Best Local Similarity: 100.0%; Pred. No.: 2.1e-203; DB ID: 424; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 Qy 1 MSYKAAGEDYKACCPPGNPAPTSNHGPATEAAEDFVDPTWTTGSAKGIDYKLIVRF 60
 1 MSYKAAGEDYKACCPPGNPAPTSNHGPATEAAEDFVDPTWTTGSAKGIDYKLIVRF 60
 Db 1 AMVHQLLIFIFTKWLQDQVNPVLVQTMDDKEYLWKDLJLTDQAYGDAVENAKDITACGF 180
 1 GSSKIDKELINRERATGQRPHHLRGTFSSHDRMNQVLDAYENKKPVLYTGRGPSE 120
 1 GSSKIDKELINRERATGQRPHHLRGTFSSHDRMNQVLDAYENKKPVLYTGRGPSE 120
 Qy 121 AMVHQLLIFIFTKWLQDQVNPVLVQTMDDKEYLWKDLJLTDQAYGDAVENAKDITACGF 180
 121 AMVHQLLIFIFTKWLQDQVNPVLVQTMDDKEYLWKDLJLTDQAYGDAVENAKDITACGF 180
 181 DINKTIFISPDLYDMGMSGPYKNTVYKIQEVTENQVKIGFTPSDCTGKSFRAOAP 240
 181 DINKTIFISPDLYDMGMSGPYKNTVYKIQEVTENQVKIGFTPSDCTGKSFRAOAP 240
 181 DINKTIFISPDLYDMGMSGPYKNTVYKIQEVTENQVKIGFTPSDCTGKSFRAOAP 240

QY 241 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 300
Db 241 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 300
QY 301 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 360
Db 301 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 360
QY 361 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 420
Db 361 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 420
QY 421 FDFO 424
Db 421 FDFO 424

RESULT 2
US-10-126-467B-2
; Sequence 2, Application US/10126467B
; Publication No. US20030059797A1
; GENERAL INFORMATION:
; APPLICANT: Paley, Elena
; FILE REFERENCE: PALL-111
; CURRENT APPLICATION NUMBER: US/10/126,467B
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,980
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/513,895
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/384,869
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-126-467B-2

Query Match 100.0%; Score 2246; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.3e-203; Mismatches 0; Indels 0; Gaps 0;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSYKAAGEDDYKADCPGPNPAPTSNHGPDATEBAEDFDWPTWQTSSAKGIDYKLIVRF 60
Db 48 MSYKAAGEDDYKADCPGPNPAPTSNHGPDATEBAEDFDWPTWQTSSAKGIDYKLIVRF 60
QY 61 GSSKIDKELINRERATGQRPHFLRGIFTSRDMNQVLDAYENKKPFYLTGRPSSE 120
Db 108 GSSKIDKELINRERATGQRPHFLRGIFTSRDMNQVLDAYENKKPFYLTGRPSSE 167
QY 121 AMVUGHJLPEITKWLQDVENPVLYIQMTDBKYLQDLTQAYDAVENAKDIIAGF 180
Db 168 AMVUGHJLPEITKWLQDVENPVLYIQMTDBKYLQDLTQAYDAVENAKDIIAGF 227
QY 181 DINKTFPSDLDMGMSSGFYKVNVKIQKHTFQNQKGIRGFTSDCIGKSPPAQAP 240
Db 228 DINKTFPSDLDMGMSSGFYKVNVKIQKHTFQNQKGIRGFTSDCIGKSPPAQAP 287
QY 241 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 300
Db 288 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 347
QY 301 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 360
Db 348 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 407
QY 361 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 420
Db 408 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 467
QY 421 FDFO 424
Db 468 FDFO 471

RESULT 3
US-09-813-718-10
; Sequence 10, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmeil, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 484
; TYPE: PRT
; FEATURE: ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: full-length TRPS in PET20B
; US-09-813-718-10

Query Match 100.0%; Score 2246; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.4e-203; Mismatches 0; Indels 0; Gaps 0;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSYKAAGEDDYKADCPGPNPAPTSNHGPDATEBAEDFDWPTWQTSSAKGIDYKLIVRF 60
Db 48 MSYKAAGEDDYKADCPGPNPAPTSNHGPDATEBAEDFDWPTWQTSSAKGIDYKLIVRF 60
QY 61 GSSKIDKELINRERATGQRPHFLRGIFTSRDMNQVLDAYENKKPFYLTGRPSSE 120
Db 108 GSSKIDKELINRERATGQRPHFLRGIFTSRDMNQVLDAYENKKPFYLTGRPSSE 167
QY 121 AMVUGHJLPEITKWLQDVENPVLYIQMTDBKYLQDLTQAYDAVENAKDIIAGF 180
Db 168 AMVUGHJLPEITKWLQDVENPVLYIQMTDBKYLQDLTQAYDAVENAKDIIAGF 227
QY 181 DINKTFPSDLDMGMSSGFYKVNVKIQKHTFQNQKGIRGFTSDCIGKSPPAQAP 240
Db 228 DINKTFPSDLDMGMSSGFYKVNVKIQKHTFQNQKGIRGFTSDCIGKSPPAQAP 287
QY 241 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 300
Db 288 SFNSNFPQIFRDRDQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALHSTFPALGAQ 347
QY 301 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 360
Db 348 TKSASDPNSISFLTDQKIKVNGAFSGGRDTIEHRQFGGNCVDVSMYLTFPL 407
QY 361 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 420
Db 408 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 467
QY 421 FDFO 424
Db 468 FDFO 471

RESULT 4
US-09-919-019-163
; Sequence 163, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; 408 EDDDKLEQTRKYDTSGAMLTGELKKALEEVQPLIHEQRKEVTDIEKEFMPRLKS 467

FILE REFERENCE: PA-0035 US
 CURRENT APPLICATION NUMBER: US/09/919,039
 PRIOR FILING DATE: 2002-09-09
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: PERL Program
 SEQ ID NO: 163
 LENGTH: 471
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. US20030108871A1 2705515CD1
 ; US-09-919-039-163

Query Match 99.3%; Score 2231; DB 9; Length 471;
 Best Local Similarity 99.5%; Pred. No. 6.2e-202; Mismatches 2; Indels 0; Gaps 0;
 Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYKAAGEDYKADCPPGNAPTSNHGPDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRF 60
 Db 52 MSYKAAGEDYKADCPPGNAPTSNHGPDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRF 111
 Qy 61 GSSKIDKELINRERATGQRPHFLRGIFSHRDMMQNVIDAYENKKPFYLYTRGPSE 120
 Db 112 GSSKIDKELINRERATGQRPHFLRGIFSHRDMMQNVIDAYENKKPFYLYTRGPSE 171
 Qy 121 AMHVGLIPLPEFTKWLQDVENVPLVQMTDEKYLWKLTDQAYDAVENAKDITACGF 180
 Db 168 AMHVGLIPLPEFTKWLQDVENVPLVQMTDEKYLWKLTDQAYDAVENAKDITACGF 227
 Qy 181 DINKTFLFSDJJDYMGMSGFYNNVKIOKHYPNQVKIGRTSDICIGKSFPAIQAP 240
 Db 228 DINKTFLFSDJJDYMGMSGFYNNVKIOKHYPNQVKIGRTSDICIGKSFPAIQAP 287
 Qy 241 SFNSNSPQIIFRDTQCLICAIQDPPYFMRDVAPRIGYKPALIHSTFPALQAO 300
 Db 288 SFNSNSPQIIFRDTQCLICAIQDPPYFMRDVAPRIGYKPALIHSTFPALQAO 347

Qy 301 TKSASADPNSSIFTDTAKQIKTKVANKHAFSGGRDTEEEHHQFGGNCDVFSMVLTFFL 360
 Db 348 TKSASADPNSSIFTDTAKQIKTKVANKHAFSGGRDTEEEHQFGGNCDVFSMVLTFFL 407

Qy 361 EDDDKLEQIRKQYTSGAMLTCBLLKALIEVQLQPLIAHQARKKEVIDEIVKEFMPRKLS 420
 Db 408 EDDDKLEQIRKQYTSGAMLTCBLLKALIEVQLQPLIAHQARKKEVIDEIVKEFMPRKLS 467

Qy 421 FDFQ 424
 Db 468 FDFQ 471

RESULT 5
 US-09-925-302-558

; Sequence 558, Application US/09925302
 ; Patent No. US20044941A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEO ID NO: 558

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-925-302-558

Query Match 99.3%; Score 2231; DB 10; Length 475;
 Best Local Similarity 99.5%; Pred. No. 6.2e-202; Mismatches 2; Indels 0; Gaps 0;
 Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSYKAAGEDYKADCPPGNAPTSNHGPDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRF 60
 Db 52 MSYKAAGEDYKADCPPGNAPTSNHGPDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRF 111
 Qy 61 GSSKIDKELINRERATGQRPHFLRGIFSHRDMMQNVIDAYENKKPFYLYTRGPSE 120
 Db 112 GSSKIDKELINRERATGQRPHFLRGIFSHRDMMQNVIDAYENKKPFYLYTRGPSE 171
 Qy 121 AMHVGLIPLPEFTKWLQDVENVPLVQMTDEKYLWKLTDQAYDAVENAKDITACGF 180
 Db 168 AMHVGLIPLPEFTKWLQDVENVPLVQMTDEKYLWKLTDQAYDAVENAKDITACGF 227
 Qy 181 DINKTFLFSDJJDYMGMSGFYNNVKIOKHYPNQVKIGRTSDICIGKSFPAIQAP 240
 Db 228 DINKTFLFSDJJDYMGMSGFYNNVKIOKHYPNQVKIGRTSDICIGKSFPAIQAP 287
 Qy 241 SFNSNSPQIIFRDTQCLICAIQDPPYFMRDVAPRIGYKPALIHSTFPALQAO 300
 Db 288 SFNSNSPQIIFRDTQCLICAIQDPPYFMRDVAPRIGYKPALIHSTFPALQAO 347

Qy 301 TKSASADPNSSIFTDTAKQIKTKVANKHAFSGGRDTEEEHHQFGGNCDVFSMVLTFFL 360
 Db 348 TKSASADPNSSIFTDTAKQIKTKVANKHAFSGGRDTEEEHQFGGNCDVFSMVLTFFL 407

Qy 361 EDDDKLEQIRKQYTSGAMLTCBLLKALIEVQLQPLIAHQARKKEVIDEIVKEFMPRKLS 420
 Db 408 EDDDKLEQIRKQYTSGAMLTCBLLKALIEVQLQPLIAHQARKKEVIDEIVKEFMPRKLS 467

Qy 421 FDFQ 424
 Db 468 FDFQ 475

RESULT 6
 US-09-813-718-14

; Sequence 14, Application US/09813718
 ; Publication No. US20020182666A1

; GENERAL INFORMATION:

; APPLICANT: Schimmel, Paul

; TITLE OF INVENTION: Human Aminocetyl-tRNA Synthetase Polypeptides Useful For File Reference: 00-221
 Current Application Number: US/09/813,718
 Current Filing Date: 2001-03-21
 Number of SEQ ID NOS: 58
 Software: PatentIn Ver. 2.0
 SEO ID NO: 14
 LENGTH: 415
 TYPE: PRT

; ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: human
 OTHER INFORMATION: supermini_TPRs in PBT20B

US-09-813-718-14

Query Match 94.2%; Score 2116; DB 9; Length 415;
 Best Local Similarity 100.0%; Pred. No. 3.6e-191; Mismatches 2; Indels 0; Gaps 0;
 Matches 401; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 SNHGDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRFQGSKIDKELINRERATGQRPH 83
 Db 2 SNHGDATAEEDFVDPWTWVOTSSAKGIDYDKLIVRFQGSKIDKELINRERATGQRPH 61

Qy 84 FLRRGIPPSRDMQNVIDAYENKKPFYLYTRGPSSSEAMAVGHJIPFTKWLQDVFNVP 143
 Db 62 FLRRGIPPSRDMQNVIDAYENKKPFYLYTRGPSSSEAMAVGHJIPFTKWLQDVFNVP 121

QY 144 LVIQMTDDEKYLWKLTDQAGDAVENAKDIACGFDINKTFISDLYMGSGFVN 203
 QY 182 VVKIQKHVTNQVKGKIGFTSDCGIKSPALQAPSNSPSQIERTDQCLICA 263
 QY 204 VKIQKHVTNQVKGKIGFTSDCGIKSPALQAPSNSPSQIERTDQCLICA 263
 Db 182 VVKIQKHVTNQVKGKIGFTSDCGIKSPALQAPSNSPSQIERTDQCLICA 241
 QY 242 IDQDPYFRTRDVARIGPKPALIISTFFPALQQTMSADPNSSTFLDTQAKQT 323
 Db 264 IDQDPYFRTRDVARIGPKPALIISTFFPALQQTMSADPNSSTFLDTQAKQT 323
 QY 302 KVNKHAFSGGRDTBEHROFGNCVDVSFMLTFFLEDDKLQBQIRDYTSGLTTEL 361
 QY 348 KALIEVLOPLIAHQARKEVTEBIVKERMTRPKLSEDFQ 424
 Do 362 KKALIEVLOPLIAHQARKEVTEBIVKERMTRPKLSEDFQ 402

RESULT 7
 US-09-813-718-15
 Sequence 16, Application US/09813718
 Publication No. US20020182666A1
 GENERAL INFORMATION:
 APPLICANT: Schimmel, Paul
 APPLICANT: Wakasugi, Keisuke
 TITLE OF INVENTION: Human Amiacyl-tRNA Synthetase Polypeptides Useful For
 TITLE OF INVENTION: The Regulation of Angiogenesis
 FILE REFERENCE: 00-221
 CURRENT APPLICATION NUMBER: US/09/813,718
 CURRENT FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 16
 LENGTH: 392
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: human minor
 ; US-09-813-718-16

Query Match 88.5%; Score 1988; DB 9; Length 392;
 Best Local Similarity 100.0%; Pred. No. 3; Ge-19; Mismatches 0; Indels 0; Gaps 0;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SAKGIDYDKLIVRGGSSKIDELINIRERATGORPHFLARRGIFPSHDMNQVDAVENK 106
 Db 2 SAKGIDYDKLIVRGGSSKIDELINIRERATGORPHFLARRGIFPSHDMNQVDAVENK 61
 QY 107 KPFYLTGKGSSRAMVHCHLITPTKMLQDVENVPLIQMTDEKYLWKLTDQY 166
 Db 62 KPFYLTGKGSSRAMVHCHLIPFKWLQDVENVPLIQMTDEKYLWKLTDQY 121
 QY 167 DAVENAKOITACGFDINKTFISDLYMGSGFYKVNQVKGKIGFTSD 226
 Db 122 DAVENAKOITACGFDINKTFISDLYMGSGFYKVNQVKGKIGFTSD 181
 QY 227 CIGKISPAIQAPSFNSFPQIFRDTRDQCLICAIDQPYFRTRDVAPRIYKPA 286
 Db 182 CIGKISPAIQAPSFNSFPQIFRDTRDQCLICAIDQPYFRTRDVAPRIYKPA 241
 QY 287 LIISTTPPALQAOGTMSASDPMNSIFLDTQAKIOTKVNQVKGKIGFTSD 346
 Db 242 LIISTTPPALQAOGTMSASDPMNSIFLDTQAKIOTKVNQVKGKIGFTSD 301
 QY 347 CDYDVSFMLTFFLEDDKLQBQIRDYTSGLTTEL 406
 Db 302 CDYDVSFMLTFFLEDDKLQBQIRDYTSGLTTEL 361

RESULT 8
 US-10-128-714-8545
 Sequence 8545, Application US/10128714
 Publication No. US20030119013A1
 GENERAL INFORMATION:
 APPLICANT: Jiang, Bo
 APPLICANT: Hu, Meng
 APPLICANT: Tishkoff, Daniel
 APPLICANT: Zamudio, Carlos
 APPLICANT: Eroshkin, Alexey M
 APPLICANT: Lemieux, Sébastien M
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 TITLE OF INVENTION: Methods of Use
 FILE REFERENCE: 10182-018-959
 CURRENT APPLICATION NUMBER: US/10/128,714
 CURRENT FILING DATE: 2002-04-23
 PRIORITY APPLICATION NUMBER: US 60/285,697
 PRIORITY FILING DATE: 2001-04-23
 PRIORITY APPLICATION NUMBER: US 60/287,066
 PRIORITY FILING DATE: 2001-04-27
 PRIORITY APPLICATION NUMBER: US 60/295,890
 PRIORITY FILING DATE: 2001-06-05
 PRIORITY APPLICATION NUMBER: US 60/303,899
 PRIORITY FILING DATE: 2001-07-09
 PRIORITY APPLICATION NUMBER: US 60/315,362
 PRIORITY FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 8603
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8545
 LENGTH: 433
 TYPE: PRT
 ORGANISM: Aspergillus fumigatus
 ; US-10-128-714-8545

Query Match 50.3%; Score 1129; DB 9; Length 433;
 Best Local Similarity 53.7%; Pred. No. 4; 4e-98; Mismatches 115; Indels 17; Gaps 7;
 Matches 227; Conservative 64; Mismatches 115; Indels 17; Gaps 7;

QY 13 ADCPGNBAPFT---SNHGDATEAEEDFVDPWTV---OTSSAKGIDYDKLIVRFGSS 63
 Do 2 ALBPGQPPLTTSLAEKAP-ASKAYAQVWPPFDVGGVDSGGVDBSGKLUPIVOKLVREFGAT 60
 QY 64 KIDKELINIRERATGORPHFLARRGIFPSHDMNQVDAVENKPPFLYTCRGPSSEAMH 123
 Do 61 RISKELLERFERVTKRPHRFMRGIVFSSHDLNLIDRYKGQPFYLTYCGRGPSSDNH 120
 QY 124 VGLHPITFKMLQDVENVPLIVQIOMTDEKYLWKLTDQY 182
 Do 121 VGTIPRFPTRMLQDVENVPLIVQIOMTDEKYLWKLTDQY 180
 QY 183 NKTFIFSDLDGMSSGFVNQVKGKIGFTSDCGIKSPALQAPS 242
 Do 181 KCFPIFSDPFG--GAFYENICRMKRITINSVCTGFENDSNNGEFHFCATQSATF 238
 QY 243 SNSPQIF-RDR---TDIQCILPCAIDQPYFRTRDVAPRIYKPA 298
 Do 239 ATSPFPFIDQCLICAIDQPYFRTRDVAPRIYKPA 298
 QY 299 ACTKMSASDPMNSIFLDTQAKIOTKVNQVKGKIGFTSD 358
 Do 299 PSSKMSASDPMNSIFLDTQAKIOTKVNQVKGKIGFTSD 358
 QY 359 FLEDDDKLQBQIRDYTSGLTTEL 418
 Do 359 FMEDESERIRVAYKEGMJTGVEKQKCIACLOAQVQFOERRAQYDTEVAEFPNRP 418
 QY 419 LSF 421

Db 419 LEW 421
 RESULT 9
 US-09-925-302-855
 ; Sequence 855, Application US/09925302
 Patent No. US2002004941A1
 GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA104
 CURRENT APPLICATION NUMBER: US/09/925,302
 CURRENT FILING DATE: 2001-08-10
 PRIORITY APPLICATION NUMBER: PCT/US00/05918
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 896
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 855
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (159)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (168)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-302-855
 Query Match 37.0%: Score 831; DB 10; Length 173;
 Best Local Similarity 98.7%; Pred. No. 1.7e-70; Matches 156; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 130 FIFTKMLQDVNPVPLVOMTDBEKYMKDUDLQDAKGDAVENAKDITACGFEDINKPPIFS 189
 Db 1 FIFTKWLQDVNPVPLVOMTDBEKYMLQDUDLQDAVSKYDINKPPIFS 60
 Qy 190 DIDYMGMSGGFKNVVKIQKHTFNOQKRGIFGPTSDCIGKISFPATQAPSFSNSPQI 249
 Db 61 DIDYGMGSQGFKNVVKIQKHTFNOQKRGIFGPTSDCIGKISFPATQAPSFSNSPQI 120
 Qy 250 FRDRTDIQCILCAIDDPYFMRTRDYAPRIGYPKPAL 287
 Db 121 FRDRTDIQCILCAIDDPYFMRTRDYAPRIGYPKPAL 158
 RESULT 10
 US-09-813-718-45
 ; Sequence 45, Application US/09813718
 ; Publication No. US20020182666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schimmel, Paul
 ; ATTORNEY: Wakasugi, Keisuke
 TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
 FILE REFERENCE: 00-221
 CURRENT APPLICATION NUMBER: US/09/813,718
 CURRENT FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 45
 LENGTH: 85
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-813-718-45
 Query Match 20.4%: Score 458; DB 9; Length 85;
 Best Local Similarity 100.0%; Pred. No. 9.5e-36; Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 11
 US-10-128-714-3545
 ; Sequence 3545, Application US/10128714
 Publication No. US20030119013A1
 GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wenqi
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Broshkin, Alexey M
 ; APPLICANT: Lemieux, Sébastien M
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and Methods of Use
 FILE REFERENCE: 10182-018-99
 CURRENT APPLICATION NUMBER: US/10/128,714
 CURRENT FILING DATE: 2002-04-23
 PRIORITY APPLICATION NUMBER: US 60/285,697
 PRIOR FILING DATE: 2001-04-23
 PRIORITY APPLICATION NUMBER: US 60/287,066
 PRIOR FILING DATE: 2001-04-27
 PRIORITY APPLICATION NUMBER: US 60/295,890
 PRIOR FILING DATE: 2001-06-05
 PRIORITY APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIORITY APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 8603
 SEQ ID NO 3545
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Aspergillus fumigatus
 ; US-10-128-714-3545
 Query Match 18.7%: Score 419; DB 9; Length 179;
 Best Local Similarity 55.7%; Pred. No. 1.3e-31; Matches 83; Conservative 21; Mismatches 35; Indels 10; Gaps 3;
 Qy 13 ADCPPENPAP---SNHGPDATEEFDYDPMWV---QTSSAKGIDYDKLIVRGSS 63
 Db 2 ADEPGOPPAALTTSLAEKAP-ASKAVAOVWTPPDVGGSVDESGKLUVPVDKLVRFGAT 60
 Qy 64 KIDKELLRNIRERATGORPHHITLRRGIFTPSHRDMNQVLDAYENKKCPYLITGRGPSEAMH 123
 Db 61 RISKEELERPRFRVTGRRHMRGIVVERSDRDLNLLDRVKGQFYLITGRGPSSDMH 120
 Qy 124 VGHLPFFTKMLQDVNPVPLVOMTDBE 152
 Db 121 VGHLPFFTKMLQDVFCPLVIMLDDE 149
 RESULT 12
 US-09-813-718-45
 ; Sequence 46, Application US/09813718
 ; Publication No. US20020182666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schimmel, Paul
 ; APPLICANT: Wakasugi, Keisuke
 TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
 FILE REFERENCE: 00-221
 CURRENT APPLICATION NUMBER: US/09/813,718
 CURRENT FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-813-718-46

Query Match 15.9%; Score 357; DB 9; Length 85;
Best Local Similarity 81.2%; Pred. No. 3.2e-26; Matches 69; Conservative 81.2%; 4; Mismatches 12; Indels 0; Gaps 0;
Matches 74; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 61
Db 2 SYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 61

RESULT 13
US-09-813-718-48
; Sequence 48, Application US/09813718
; Publication No. US2002012666A1

; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813, 718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-09-813-718-48

Query Match 16.2%; Score 363; DB 9; Length 85;
Best Local Similarity 82.4%; Pred. No. 8.7e-27; Matches 70; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

Qy 2 SYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 60
Db 2 SYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 60

Qy 61 GSSKIDKELNIRERATGQRPHFL 85
Db 61 GSSKIDKELNIRERATGQRPHFL 85

RESULT 14
US-09-813-718-47
; Sequence 47, Application US/09813718
; Publication No. US2002012666A1

; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813, 718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-813-718-47

Query Match 15.9%; Score 357; DB 9; Length 85;
Best Local Similarity 81.2%; Pred. No. 3.2e-26; Matches 69; Conservative 81.2%; 4; Mismatches 12; Indels 0; Gaps 0;
Matches 74; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MSYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 60
Db 1 MSYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 60

Qy 61 GSSKIDKELNIRERATGQRPHFL 85
Db 61 GSSKIDKELNIRERATGQRPHFL 85

RESULT 15
US-09-925-302-557
; Sequence 557, Application US/09925302
; Patent No. US20020044941A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/9/925, 302
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05918

; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124, 270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 557
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (130)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (142)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-302-557

Query Match 15.9%; Score 356.5; DB 10; Length 142;
Best Local Similarity 78.0%; Pred. No. 7.5e-26; Matches 71; Conservative 78.0%; 5; Mismatches 12; Indels 3; Gaps 2;

Qy 1 MSYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 60
Db 52 MSYKAAGAEDYKACDCPPGNPAPTSNHPGDATEAEEDFVDPWTQISSAKGIDYDYLIVRF 111

Qy 61 GSSKIDKELNIRERATGQRPHFL 91
Db 112 GSSXNKXELLXDXE-STAKXHS--GQGXFF 139

Search completed: July 10, 2003, 12:33:36
Job time : 22.5855 sec

XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction - Disclosure; Page 122-24; 150pp; English.

XX The sequences given in AAB47615-18 show full length and truncated versions of trypophanyl-tRNA synthetase (Trps). The truncated Trps of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length Trps with polymorphonuclear leucocyte elastase. Truncated Trps is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumour, and condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated Trps promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polyribonucleotides directly to the lumen and wall of the blood vessel.

XX Sequence 437 AA;

Query Match 100.0%; Score 2246; DB 22; Length 437;
Best Local Similarity 100.0%; Pred. No. 7, 4e-222; Mismatches 0; Indels 0; Gaps 0;
Matches 424; Conservative 0;

QY 1 MSYKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
1 MSTKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
61 GSSKIDKELINRERATQRPHRLRGCFERFRHDMQVLDAYENKKPFYLITGRGPSE 120
61 GSSKIDKELINRERATQRPHRLRGCFERFRHDMQVLDAYENKKPFYLITGRGPSE 120
121 AMVGHALPPFLQVNPVNLQVMTDCEYLKQLTQAYGAVENAKDIAGF 180
121 AMVGHALPPFLQVNPVNLQVMTDCEYLKQLTQAYGAVENAKDIAGF 180
181 DINKTFIFSDLQYMGMSGFQYKVKQKHTVNQKGIGFGTDSDCIGKISPAQAP 240
181 DINKTFIFSDLQYMGMSGFQYKVKQKHTVNQKGIGFGTDSDCIGKISPAQAP 240
Db 241 SFNSNSFPQIPIFRDTRIOCLIPCAIDQDFYFRMTRDVAFPRIGYKPKALHSTFPALQAO 300
Db 301 TKSASDENSISFLTDQKTKVKAQFSGRDTRIEHRDQGGNCVWDVSNLYTFL 360
Db 361 EDDDKLEQTRKDITSGAMLTGELKKALIEVLQPLAERQARREGEVDIKEVMPRKLS 420
Db 361 EDDDKLEQTRKDITSGAMLTGELKKALIEVLQPLAERQARREGEVDIKEVMPRKLS 420
QY 421 FDFQ 424
Db 421 FDFQ 424

SQ Sequence 437 AA;

Query Match 100.0%; Score 2246; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 7, 4e-222; Mismatches 0; Indels 0; Gaps 0;
Matches 424; Conservative 0;

QY 1 MSYKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
1 MSTKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
61 GSSKIDKELINRERATQRPHRLRGCFERFRHDMQVLDAYENKKPFYLITGRGPSE 120

XX Human mini tryptophanyl t-RNA synthetase in PET20B.
XX Human: trypophanyl-tRNA synthetase; Trps; tyrosyl t-RNA synthetase;
KW TYRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
XX Homo sapiens.
XX WO200175078-A1.
XX 11-OCT-2001.
XX 21-MAR-2001; 2001WO-US08975.
XX 31-MAR-2000; 2000US-193471P.
XX (SCRI) SCRIPPS RES INST.
XX PI Schimmel P, Wakasugi K;
XX DR N-PSDB; AAB22483.
XX WPI; 2002-010784/01.
XX DR
PS Example 1; Page 123-124; 149pp; English.
XX The patient discloses human aminoacyl tRNA synthetases, particularly truncated trypophanyl-tRNA synthetases (Trps) comprising a Rossmann fold nucleotide binding domain and polyribonucleotides encoding them. The invention also relates to tyrosyl t-RNA synthetases (Tyrs). Trps sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic Trps sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. Trps sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogen Trps is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. Trps is also used in conjunction with angiography. Trps DNAs are useful in gene therapy. Trps antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of Trps by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human truncated trypophanyl t-RNA synthetase (mini Trps; residues 48-471 of full-length Trps protein) protein in pET20B.

XX Sequence 437 AA;

Query Match 100.0%; Score 2246; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 7, 4e-222; Mismatches 0; Indels 0; Gaps 0;
Matches 424; Conservative 0;

QY 1 MSYKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
1 MSTKAAGEDYKADCPGNPAPTSNHGDATEAEDFDPMWVOTSSAKGIDYDKLIVRF 60
61 GSSKIDKELINRERATQRPHRLRGCFERFRHDMQVLDAYENKKPFYLITGRGPSE 120

RESULT 2
RAE13492
ID AAE13492 standard; Protein; 437 AA.
XX AAB13492;
AC
DR 12-FEB-2002 (first entry)

Db 61 GSSKIDKELINRERATGQRPHFLRGIFPFHRDMQVDAVENKKPFLYLTGRGPSE 120
 Qy AMHVGHLIPFTIKWLDQFVNPFVPLVQTMDDDEKYLWKLTDQAYGDAVENAKDITACGF 180
 Db 121 AMHVGHLIPFTIKWLDQFVNPFVPLVQTMDDDEKYLWKLTDQAYGDAVENAKDITACGF 180
 Qy 181 DINKTIFPSDDYGMSSGFYKVVKIQRHVTNQVKIGFGFDSDCIGKISFPATQAP 240
 Db 181 DINKTIFPSDDYGMSSGFYKVVKIQRHVTNQVKIGFGFDSDCIGKISFPATQAP 240
 Qy 241 SFSNSFQIFRTRDIFLQCLIPAKOQIPIAODPYFRMTRDVAPRIGPKPAIHSPPALOGAQ 300
 Db 241 SFSNSFQIFRTRDIFLQCLIPAKOQIPIAODPYFRMTRDVAPRIGPKPAIHSPPALOGAQ 300
 Qy 301 TMSASDPNNSIFLTDQAKOQTKVVKHAFSGRDTBEHRQGGNCVDVSPMLTFEL 360
 Db 301 TMSASDPNNSIFLTDQAKOQTKVVKHAFSGRDTBEHRQGGNCVDVSPMLTFEL 360
 Qy 361 EDDDKLQIRKDYTSGAMLGELKKALIEVLOPLIAEHOARKETDEIVKEFMPRLKS 420
 Db 361 EDDDKLQIRKDYTSGAMLGELKKALIEVLOPLIAEHOARKETDEIVKEFMPRLKS 420
 Qy 421 FDFQ 424
 Db 421 FDFQ 424

RESULT 3

ID AAB47615
 ID AAB47615 standard; Protein: 484 AA.
 AC AAB47615;
 XX DT 07-JAN-2002 (first entry)
 XX DE Human full-length Trprs.
 XX KW Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain;
 XX vascular endothelial cell function; burn; plastic surgery; abdomen;
 XX KW Polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
 XX angiogenesis; graft; myocardial infarction; solid tumour; wound healing;
 XX dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; tprRS; vascular graft surgery.
 OS Homo sapiens.
 XX PN WO200174841-A1.
 XX PD 11-OCT-2001.
 XX PR 21-MAR-2001; 2001WO-US08965.
 PR 31-MAR-2000; 2000US-193471P.

XX PA (SCRIPPS RES INST.
 XX PI Schimmel P, Wakasugi K;
 XX DR WPI; 2001-626377/72.
 DR N-PSDB; AAB43602.

XX PT New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis, and treating myocardial infarction - Disclosure; Page 117-19; 150pp; English.

XX CC The sequences given in AAB47615-18 show full length and truncated versions of tryptophanyl-tRNA synthetase (Trprs). The truncated Trprs of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of

CC full length Trprs with polymorphonuclear leucocyte elastase. Truncated Trprs is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated Trprs promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel.

SQ Sequence 484 AA; Query Match 100 %; Score 246; DB 22; Length 484; Best Local Similarity 100 %; Pred. No. 8.7e-22; Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC

AC 1 MSYKAAGEDYKADCPGPNNPAPTSNGPDATEAEEDFVDPMTVQTSKAGIDYDYLVRP 60
 AC 108 GSSKIDKELINRERATGQRPHFLRGIFPSHRDNQVDAVENKKPFLYLTGRGPSE 167
 Qy 121 AMHVGHLIPFTIKWLDQFVNPFVPLVQTMDDDEKYLWKLTDQAYGDAVENAKDITACGF 180
 Db 168 AMHVGHLIPFTIKWLDQFVNPFVPLVQTMDDDEKYLWKLTDQAYGDAVENAKDITACGF 227
 Qy 181 DINKTIFPSDDYGMSSGFYKVVKIQRHVTNQVKIGFGFDSDCIGKISFPATQAP 240
 Db 181 DINKTIFPSDDYGMSSGFYKVVKIQRHVTNQVKIGFGFDSDCIGKISFPATQAP 240
 Qy 228 DINKTIFPSDDYGMSSGFYKVVKIQRHVTNQVKIGFGFDSDCIGKISFPATQAP 287
 Db 288 SFSNSFQIFRTRDIFLQCLIPAKOQIPIAODPYFRMTRDVAPRIGPKPAIHSPPALOGAQ 347
 Qy 301 TMSASDPNNSIFLTDQAKOQTKVVKHAFSGRDTBEHRQGGNCVDVSPMLTFEL 360
 Db 348 TMSASDPNNSIFLTDQAKOQTKVVKHAFSGRDTBEHRQGGNCVDVSPMLTFEL 407
 Qy 361 EDDDKLQIRKDYTSGAMLGELKKALIEVLOPLIAEHOARKETDEIVKEFMPRLKS 420
 Db 408 EDDDKLQIRKDYTSGAMLGELKKALIEVLOPLIAEHOARKETDEIVKEFMPRLKS 467
 Qy 421 FDFQ 424
 Db 468 FDFQ 471

RESULT 4

ID AAE13491
 ID AAE13491 standard; Protein: 484 AA.
 AC AAE13491;
 XX DR 12-FEB-2002 (first entry)
 XX DE Human tryptophanyl t-RNA synthetase (Trprs) in pET20B.
 XX KW Human; tryptophanyl-tRNA synthetase; Trprs; tyrosyl t-RNA synthetase; Trprs; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.

XX OS Homo sapiens.

XX

PN WO200175078-A1.
 XX PD 11-OCT-2001.
 XX PR 21-MAR-2001; 2001WO-US08975.
 XX PR 31-MAR-2000; 2000US-193471P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Schimmel P, Wakasugi K;
 DR WPI; 2002-010784/01.
 DR N-PSDB; AAB22482.
 XX PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of
 PT regulating vascular endothelial cell function, preferably angiogenesis,
 PT is useful for treating solid tumor or suppressing tumor metastasis in
 PT mammal -
 PS Example 1; Page 117-119; 149pp; English.
 XX CC The patient discloses human aminoacyl tRNA synthetase, particularly
 CC truncated tryptophanyl-tRNA synthetases (TrRS) comprising a Rossmann
 CC fold nucleotide binding domain and polynucleotides encoding them. The
 CC invention also relates to tyrosyl t-RNA synthetases (TyRS). TrRS
 CC sequences are also useful for regulating vascular endothelial cell function,
 CC preferably angiogenesis. Angiogenic TrRS sequences are useful as wound
 CC healing agents for re-vascularising damaged tissues. They are useful for
 CC treating full-thickness wounds (e.g. dermal ulcers), including pressure
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrRS
 CC sequences can also be used in plastic surgery when reconstruction is
 CC required following a burn, other trauma, or even for cosmetic purposes.
 CC Angiogenic TrRS is also used in association with surgery and following
 CC the repair of cuts, for promoting endothelialisation in vascular graft
 CC surgery and for repairing the damage of myocardial infarction and in
 CC conjunction with coronary bypass surgery by stimulating the growth of
 CC transplanted tissue. TrRS is also used in conjunction with angiography.
 CC TrRS DNAs are useful in gene therapy. TrRS antibodies are used in
 CC immunoassays to detect the presence of tumours. They are also useful
 CC for blocking endogenous angiogenic activity and retard the growth of
 CC solid tumours. These antibodies may also be used to treat inflammation
 CC caused by increased vascular permeability. Inhibiting the activity of
 CC TrRS by antisense technology is useful for preventing further growth
 CC or even regress solid tumours, and for treating rheumatoid arthritis,
 CC psoriasis, diabetic retinopathy, all of which are characterised by
 CC abnormal angiogenesis. The present sequence is human tryptophanyl
 CC t-RNA synthetase (TrRS) in pBT20B.
 XX Sequence 484 AA:
 SQ Query Match 100.0%; Score 2246; DB 23; Length 484;
 Best Local Similarity 100.0%; Pred. No. 8; Je-222;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX PT Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer -
 XX PS Claim 11; Page 1052-1053; 1425pp; English.
 XX Polynucleotide sequences AF17982 - AF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB5648. Lung cancer
 CC associated proteins and Polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytostatic; cardioactive;
 CC immunomodulatory; muscarinic active general; vulnerary; gastrointestinal
 CC general; nephrotoxic; anti-infective; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the
 CC protein or polynucleotide sequences. The lung cancer associated
 CC polynucleotide sequences may be used for detection of lung cancer,
 CC chromosome identification, as chromosome markers, and for numerous other
 CC diagnostic or research purposes. The proteins may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders. The proteins may also be used in the treatment of wounds and
 CC infectious diseases. Polynucleotide sequences AF18425 - AAF18433 and
 CC peptide AAB5849 are used in the course of the invention for the
 CC identification and characterisation of the polynucleotide and protein
 sequences.

DB 288 SFNSNFPQIFRRTD1QCLICPAIDQDPYFRMTDVAPPARYKPALLHSTFPALGAQ 347
 QY 301 TKSASPPNSFLTDPAKQIKTKVNHAFSGCRDTEERHOFGNCDDVSFMYLTFL 360
 DB 348 TKSASPDNSSFUTDPAKQIKTKVNHAFSGCRDTEERHOFGNCDDVSFMYLTFL 407
 QY 361 EDDKLEQIRKOTSGAMLTGELKKALAEVLOPLAERQARKEVDEIVKFMTPLKLS 420
 DB 408 EDDKLEQIRKOTSGAMLTGELKKALAEVLOPLAERQARKEVDEIVKFMTPLKLS 467
 QY 421 FD5Q 424
 DB 468 FD5Q 471

XX
PD 11-OCT-2001.
XX
PF 21-MAR-2001; 2001WO-US08966.
XX
PR 31-MAR-2000; 2000US-193471P.
XX
PA (SCRIPPS RBS INST.
PI Schimmel P, Wakasugi K;
XX DR WPI; 2001-626377/72.
DR N-PSDB; AAH43604.

XX
PT New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis, and treating myocardial infarction - disclosure; Page 129-30; 150pp; English.

XX
CC The sequences given in AAB7615-18 show full length and truncated versions of tryptophanyl-tRNA Synthetase (TrPRS). The truncated TrPRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrPRS with polymorphonuclear leucocyte elastase. Truncated TrPRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrPRS promotes endothelialisation in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA in CC conjunction with angiography to administer the angiogenic tRNA CC wall of the blood vessel.

XX
SQ Sequence 415 AA;

Query Match 94.2%; Score 2116; DB 22; Length 415;
Best Local Similarity 100.0%; Prd. No. 1.6e-208; Matches 401; Conservancy 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 SNHQPDATAEAEEDVDPWTQTSAAKGDYDYLIVRFGSSKIDKELINIERATGQRPH 83
Db 2 SNHQPDATAEAEEDVDPWTQTSAAKGDYDYLIVRFGSSKIDKELINIERATGQRPH 61
QY 84 FLRGIGFFSHRMNQVLDAYENKECPYLITGRGSSEAMHVGHLIPPTKMQDVENV 143
Db 62 FLRGIGFFSHRMNQVLDAYENKECPYLITGRGSSEAMHVGHLIPPTKMQDVENV 121
QY 144 LVIQMTDESKYIWLKDLTQAVGDAVENAKDIIAGFDINKTFESDADYMMMSGYKN 203
Db 122 LVQMTDDESKYIWLKDLTQAVGDAVENAKDIIAGFDINKTFESDADYMMMSGYKN 181
QY 204 VKLQKHVTQNVKGIGTSDCGIKSPPAQLQAPSFSNISFQIFRDTQCLPCA 263
Db 182 VKLQKHVTQNVKGIGTSDCGIKSPPAQLQAPSFSNISFQIFRDTQCLPCA 241
QY 264 IDQDPYFRMTRDVAAPRIGPKPALIHSSTPPALOGAQTKMSASDPNSSTFLTDQAKQT 323
Db 242 IDQDPYFRMTRDVAAPRIGPKPALIHSSTPPALOGAQTKMSASDPNSSTFLTDQAKQT 301
QY 324 KUNKHAFSGGRDTIEBHQFGNCQDVSFPMYLTFLEDDKUBQIRDYTSQMLGEL 383
Db 302 KUNKHAFSGGRDTIEBHQFGNCQDVSFPMYLTFLEDDKUBQIRDYTSQMLGEL 361
QY 384 KALIEVLOPLIAHQARKEVTEBIVKFMPKLSFDPQ 424
Db 362 KALIEVLOPLIAHQARKEVTEBIVKFMPKLSFDPQ 402

XX
PS Example 1; Page 129-130; 149pp; English.

XX
CC The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrPRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to Tyrosyl t-RNA Synthetases (TyRS). TrPRS sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrPRS sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrPRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrPRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrPRS is also used in conjunction with angiography. TrPRS DNAs are useful in gene therapy. TrPRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenin activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrPRS by antisense technology is useful for preventing further growth or even regressing solid tumors, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human truncated tryptophanyl t-RNA synthetase (supermini TrPRS; residues 71-471 of full-length TrPRS protein) in PBT20B.

XX
SQ Sequence 415 AA;

RESULT 8
ID AAB13493
ID AAB13493 standard; Protein; 415 AA.
AC AAB13493;
XX
DE Human supermini tryptophanyl t-RNA synthetase in PBT20B.
KW Human; tryptophanyl-tRNA synthetase; TrPRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcers; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
XX
OS Homo sapiens.
PN WO200175078-A1.
XX
PD 11-OCT-2001.
XX
PF 21-MAR-2001; 2001WO-US08975.
XX
PR 31-MAR-2000; 2000US-193471P.
XX
PA (SCRIPPS RBS INST.
XX
PI Schimmel P, Wakasugi K;
XX DR WPI; 2002-010784/01.
DR N-PSDB; AAD22484.
XX
PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in mammal -
PT
XX
PS Example 1; Page 129-130; 149pp; English.

XX
CC The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrPRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to Tyrosyl t-RNA Synthetases (TyRS). TrPRS sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrPRS sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrPRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrPRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrPRS is also used in conjunction with angiography. TrPRS DNAs are useful in gene therapy. TrPRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenin activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrPRS by antisense technology is useful for preventing further growth or even regressing solid tumors, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human truncated tryptophanyl t-RNA synthetase (supermini TrPRS; residues 71-471 of full-length TrPRS protein) in PBT20B.

Query Match 94.2%; Score 2116; DB 23; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1. 6e-208; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SNIGPDATEAEEDFVDPWVQSSAKGIDYDYLKUVRGSSSKIDKELENRERATGORPHH 83
 Db 2 SNIGPDATEAEEDFVDPWVQSSAKGIDYDYLKUVRGSSSKIDKELENRERATGORPHH 83

Qy 84 FURGGIFFSHRDMDNQVDAHENKKPPVLYTGRPSSEAMWHQLIPFPTKMDQDVENP 143
 Db 62 FURGGIFFSHRDMDNQVDAHENKKPPVLYTGRPSSEAMWHQLIPFPTKMDQDVENP 121

Qy 144 LVIQMTDEKYLWMDLTDQAGDAVENAKDTACGPDKINKPFIISPDLSLDYGMMSGYKN 203
 Db 122 LVIQMTDEKYLWMDLTDQAGDAVENAKDTACGPDKINKPFIISPDLSLDYGMMSGYKN 181

Qy 204 VKLQKHVFNQVKGIGFTSDCIGKTSPPATOQAPSFSNSNPQIIFRDRDIOCLPCA 263
 Db 182 VKLQKHVFNQVKGIGFTSDCIGKTSPPATOQAPSFSNSNPQIIFRDRDIOCLPCA 241

Qy 264 IDDOPPYFRMTRDVAPRIGYPKPAHLSTFPALQAGTQKMSASPDNSPIFLDTAKOIKT 323
 Db 242 IDDOPPYFRMTRDVAPRIGYPKPAHLSTFPALQAGTQKMSASPDNSPIFLDTAKOIKT 301

Qy 324 KVNKAHSGGRTTEHRQFGNCNDVSPMIFTFLEDDDKLEQIRKDYSGAMLGEL 383
 Db 302 KVNKAHSGGRTTEHRQFGNCNDVSPMILTFLEDDDKLEQIRKDYSGAMLGEL 361

Qy 384 KUAKIEVNLQPLAHEQARKEVDEIVKEFMPTRKLUSFDQ 424
 Db 362 KUAKIEVNLQPLAHEQARKEVDEIVKEFMPTRKLUSFDQ 402

RESULT 9

ID AAB47618 standard; Protein: 392 AA.
 AC AAB47618;
 DT 07-JAN-2002 (first entry)
 XX Human inactive TrPRS.

XX Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trPRS; vascular graft surgery.

OS Homo sapiens.
 XX W0200174841-A1.
 XX PD 11-OCT-2001.
 XX PP 21-MAR-2001; 2001WO-US08956.
 XX PR 31-MAR-2000; 2000US-193471P.
 PA (SCRIPPS RES INST.
 XX PT Schimmel P, Wakasugi K;
 DR WPI; 2001-626377/72.
 DR N-PSDB; AAB43605.

XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction - Disclosure; Page 135-36; 150pp; English.

PS

Sequence 392 AA;

Query Match 88.5%; Score 1988; DB 22; Length 392;
 Best Local Similarity 100.0%; Pred. No. 2. 2e-15; Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 SAKGIDYDYLKUVRGSSSKIDKELENRERATGORPHHFLRGIFSHRDMDNQVDAHENK 106
 Db 2 SAKGIDYDYLKUVRGSSSKIDKELENRERATGORPHHFLRGIFSHRDMDNQVDAHENK 61

Qy 107 KEPFYLTGRGESSEAMWHQLIPFPTKMDQDVENP 166
 Db 62 KEPFYLTGRGESSEAMWHQLIPFPTKMDQDVENP 121

Qy 167 DAVENAKDTACGPDKINKPFIISPDLSLDYGMMSGYKNVKLQKHVFNQVKGIGFTSD 226
 Db 122 DAVENAKDTACGPDKINKPFIISPDLSLDYGMMSGYKNVKLQKHVFNQVKGIGFTSD 181

Qy 227 CIGKTSPPATOQAPSFSNSNPQIIFRDRDIOCLPCAIDDOPPYFRMTRDVAPRIGYPK 286
 Db 182 CIGKTSPPATOQAPSFSNSNPQIIFRDRDIOCLPCAIDDOPPYFRMTRDVAPRIGYPK 241

Qy 287 LHSTFPALQAGTQKMSASPDNSPIFLDTAKOIKTAKVNGHAFSGGRDTTEHRQFGN 346
 Db 242 LHSTFPALQAGTQKMSASPDNSPIFLDTAKOIKTAKVNGHAFSGGRDTTEHRQFGN 301

Qy 347 CDDVDSFMILTFLEDDDKLEQIRKDYSGAMLGELKUAKIEVNLQPLAHEQARKEVT 406
 Db 302 CDDVDSFMILTFLEDDDKLEQIRKDYSGAMLGELKUAKIEVNLQPLAHEQARKEVT 361

Qy 407 DREVKEFMPTRKLUSFDQ 424
 Db 362 DREVKEFMPTRKLUSFDQ 379

RESULT 10

AAE1494
 ID AAE1494 standard; Protein: 392 AA.
 XX
 AC AAE1494;
 XX DT 12-FEB-2002 (first entry)
 XX DE Human inactive tryptophanyl t-RNA synthetase in PET20B.
 XX Human; tryptophanyl-tRNA synthetase; TrPRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.

OS Homo sapiens.

XX WO200175078-A1.
 XX PD 11-OCT-2001.
 XX PR 21-MAR-2001; 2001WO-US08975.
 XX PR 31-MAR-2000; 2000US-193471P.
 XX PA (SCRIPPS RES INST.
 XX PI Schimmel P, Wakasugi K;
 XX DR WPI; 2002-010784/01.
 XX N-PSDB; AAD2485.
 PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of
 PT regulating vascular endothelial cell function, preferably angiogenesis,
 PT is useful for treating solid tumor or suppressing tumor metastasis in
 PT mammal -
 PS disclosure; Page 135-136; 149pp; English.
 XX The parent disclosure human aminoacyl tRNA synthetases, particularly
 CC truncated tryptophanyl-tRNA synthetases (Trps), comprising a Rossmann
 CC fold nucleotide binding domain and polynucleotides encoding them. The
 CC invention also relates to tyrosyl t-RNA synthetases (TyrS). Trps
 CC sequences are useful for regulating vascular endothelial cell function,
 CC preferably angiogenesis. Angiogenic Trps sequences are useful as wound
 CC healing agents for re-vascularising damaged tissues. They are useful for
 CC treating full-thickness wounds (e.g. dermal ulcers, including pressure
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. Trps
 CC sequences can also be used in plastic surgery when reconstruction is
 required following a burn, other trauma, or even for cosmetic purposes.
 CC Angiogenic Trps is also used in association with surgery and following
 CC the repair of cuts, for promoting endothelialization in vascular graft
 CC surgery, and for repairing the damage of myocardial infarction and in
 CC conjunction with coronary bypass surgery by stimulating the growth of
 CC transplanted tissue. Trps is also used in conjunction with angiography.
 CC Trps DNAs are useful in gene therapy. Trps antibodies are used in
 CC immunoassays to detect the presence of tumours. They are also useful
 CC for blocking endogenous angiogenic activity and retard the growth of
 CC solid tumours. These antibodies may also be used to treat inflammation
 CC caused by increased vascular permeability. Inhibiting the activity of
 CC Trps by antisense technology is useful for preventing further growth
 CC or even regress solid tumours, and for treating rheumatoid arthritis,
 CC psoriasis, diabetic retinopathy, all of which are characterised by
 CC abnormal angiogenesis. The present sequence is human inactive
 CC tryptophanyl t-RNA synthetase (Trps) in pBT20B.
 XX Sequence 392 AA;

Query Match 88.5%; Score 1988; DB 23; Length 392;
 Best Local Similarity 100.0%; Pred. No. 2; 2e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 378; Conservative 0;

Qy 47 SAKGKDYDKLIVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENK 106
 Db 2 SAKGKDYDKLIVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENK 61

Qy 107 KPFYLTERGPSSRMYHGLIPITFKWQDVENPVLIQMTDEDKYLWQDITLDDQYG 166
 Db 62 KPFYLTYLGRGPSSRMYHGLIPITFKWQDVENPVLIQMTDEDKYLWQDITLDDQYG 121

Qy 167 DAVENAKDITACCGDINKTPFISDLYGMMSGKYKVKIQLKETVFMQVKGIFGFTSD 226
 Db 122 DAVENAKDITACGFDINKTPFISDLYGMMSGKYKVKIQLKETVFMQVKGIFGFTSD 181

Qy 227 CIGKISFPQIAQRSFSNSFPQFRDRDIOCLICPAIDQDPYRMRTRDVAQPRIGYKPA 286
 Db 182 CIGKISFPQIAQRSFSNSFPQFRDRDIOCLICPAIDQDPYRMRTRDVAQPRIGYKPA 241

Qy 287 LHSTPPPALQGAQTKMSASDPNSSIIFTDTAKIKTKVKAFASSGRDTIBERHQRFGN 346

XX Sequence 11 AA;

Query Match 61.4%; Score 1378; DB 22; Length 430;
 Best Local Similarity 61.4%; Pred. No. 1; 3e-132; Mismatches 85; Indels 16; Gaps 3;
 Matches 262; Conservative 64; Mismatches 85; Indels 16; Gaps 3;

Qy 10 DYKADCPGPNPAPTSNHGPD-----TEA-----EDFVDPWTQPTSSAKGIDYD 54
 Db 3 DTKEFVWGVGEAULTNGKPDAPSEVETGIDAQMEGATAPTEDVDPWNVASSNDAGVYD 62

Qy 55 KLVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENKPPVITYG 114

Do 242 LKHSSTPPPALQGAQTKMSASDPNSSIIFTDTAKIKTKVKAFASSGRDTIBERHQRFGN 301
 Do 347 CDVDVSENMLTFPLEDDDKLEQIRKQDVTSGAMLTGKJALKTEVQPLIAHQARKVENT 406
 Qy 302 CDVDSFVNLTFPLEDDDKLEQIRKQDVTSGAMLTGKJALKTEVQPLIAHQARKVENT 361
 Do 407 DELVKEFNTPRKLSFDQ 424
 Qy 362 DELVKEFNTPRKLSFDQ 379

RESULT 11
 XX ABB64621
 ID ABB64621 standard; Protein; 430 AA.
 XX AC ABB64621;
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 20655.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX Drosophila melanogaster.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 20655.
 XX KW pharmaceutical.
 XX PA (PEKE) PE CORP NY.
 XX XE 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX XE Venter JC, Adams M, Li PW, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX N-PSDB; ABLO8724.

XX Sequence 392 AA;

Query Match 88.5%; Score 1988; DB 23; Length 392;
 Best Local Similarity 100.0%; Pred. No. 2; 2e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 378; Conservative 0;

Qy 47 SAKGKDYDKLIVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENK 106
 Db 2 SAKGKDYDKLIVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENK 61

Qy 107 KPFYLTERGPSSRMYHGLIPITFKWQDVENPVLIQMTDEDKYLWQDITLDDQYG 166
 Db 62 KPFYLTYLGRGPSSRMYHGLIPITFKWQDVENPVLIQMTDEDKYLWQDITLDDQYG 121

Qy 167 DAVENAKDITACCGDINKTPFISDLYGMMSGKYKVKIQLKETVFMQVKGIFGFTSD 226
 Db 122 DAVENAKDITACGFDINKTPFISDLYGMMSGKYKVKIQLKETVFMQVKGIFGFTSD 181

Qy 227 CIGKISFPQIAQRSFSNSFPQFRDRDIOCLICPAIDQDPYRMRTRDVAQPRIGYKPA 286
 Db 182 CIGKISFPQIAQRSFSNSFPQFRDRDIOCLICPAIDQDPYRMRTRDVAQPRIGYKPA 241

Qy 287 LHSTPPPALQGAQTKMSASDPNSSIIFTDTAKIKTKVKAFASSGRDTIBERHQRFGN 346

XX Sequence 11 AA;

Query Match 61.4%; Score 1378; DB 22; Length 430;
 Best Local Similarity 61.4%; Pred. No. 1; 3e-132; Mismatches 85; Indels 16; Gaps 3;
 Matches 262; Conservative 64; Mismatches 85; Indels 16; Gaps 3;

Qy 10 DYKADCPGPNPAPTSNHGPD-----TEA-----EDFVDPWTQPTSSAKGIDYD 54
 Db 3 DTKEFVWGVGEAULTNGKPDAPSEVETGIDAQMEGATAPTEDVDPWNVASSNDAGVYD 62

Qy 55 KLVRGSSKIDKEKLNRERATGQPHFHFLRGGFFSHRDMDNQVLDAYENKPPVITYG 114

PR	16-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR	19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	99US-0130891.	PR	21-JUL-1999;	99US-0144884.
PR	26-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-014814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR	04-MAY-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR	07-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR	10-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145218.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134218.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134219.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134221.	PR	27-JUL-1999;	99US-0145918.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145919.
PR	18-MAY-1999;	99US-0134768.	PR	28-JUL-1999;	99US-0145931.
PR	19-MAY-1999;	99US-0134941.	PR	02-AUG-1999;	99US-0146386.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146388.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146389.
PR	24-MAY-1999;	99US-0135629.	PR	03-AUG-1999;	99US-0147038.
PR	25-MAY-1999;	99US-0136021.	PR	04-AUG-1999;	99US-0147204.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147302.
PR	28-MAY-1999;	99US-01368540.	PR	05-AUG-1999;	99US-0147192.
PR	01-JUN-1999;	99US-0136782.	PR	05-AUG-1999;	99US-017260.
PR	01-JUN-1999;	99US-0138847.	PR	06-AUG-1999;	99US-0147303.
PR	14-JUN-1999;	99US-0139119.	PR	06-AUG-1999;	99US-0147416.
PR	16-JUN-1999;	99US-0139452.	PR	09-AUG-1999;	99US-0147493.
PR	07-JUN-1999;	99US-0137724.	PR	10-AUG-1999;	99US-0148171.
PR	08-JUN-1999;	99US-0138094.	PR	11-AUG-1999;	99US-0148319.
PR	10-JUN-1999;	99US-0138540.	PR	12-AUG-1999;	99US-0148341.
PR	10-JUN-1999;	99US-0138847.	PR	13-AUG-1999;	99US-0148365.
PR	14-JUN-1999;	99US-0137222.	PR	16-AUG-1999;	99US-0149366.
PR	16-JUN-1999;	99US-0137528.	PR	17-AUG-1999;	99US-0149175.
PR	04-JUN-1999;	99US-0137502.	PR	18-AUG-1999;	99US-0149426.
PR	07-JUN-1999;	99US-0137724.	PR	20-AUG-1999;	99US-0149722.
PR	08-JUN-1999;	99US-0138094.	PR	20-AUG-1999;	99US-0149733.
PR	10-JUN-1999;	99US-0138540.	PR	27-AUG-1999;	99US-0149229.
PR	10-JUN-1999;	99US-0138847.	PR	27-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139455.	PR	23-AUG-1999;	99US-0149900.
PR	18-JUN-1999;	99US-0139456.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139457.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139458.	PR	27-AUG-1999;	99US-0151065.
PR	17-JUN-1999;	99US-0139459.	PR	27-AUG-1999;	99US-0151066.
PR	18-JUN-1999;	99US-0139454.	PR	27-AUG-1999;	99US-0151080.
PR	18-JUN-1999;	99US-0139461.	PR	30-AUG-1999;	99US-015103.
PR	18-JUN-1999;	99US-0139462.	PR	31-AUG-1999;	99US-0151438.
PR	18-JUN-1999;	99US-0139463.	PR	01-SEP-1999;	99US-0151920.
PR	18-JUN-1999;	99US-0139750.	PR	07-SEP-1999;	99US-015263.
PR	18-JUN-1999;	99US-0139763.	PR	10-SEP-1999;	99US-0153070.
PR	20-JUN-1999;	99US-0139817.	PR	13-SEP-1999;	99US-0153758.
PR	22-JUN-1999;	99US-0139899.	PR	15-SEP-1999;	99US-0154018.
PR	23-JUN-1999;	99US-0140353.	PR	16-SEP-1999;	99US-0154039.
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PR	24-JUN-1999;	99US-0140695.	PR	22-SEP-1999;	99US-0155139.
PR	28-JUN-1999;	99US-0140823.	PR	23-SEP-1999;	99US-0155486.
PR	29-JUN-1999;	99US-0140991.	PR	24-SEP-1999;	99US-0155659.
PR	30-JUN-1999;	99US-0141287.	PR	28-SEP-1999;	99US-0156358.
PR	01-JUL-1999;	99US-0141842.	PR	29-SEP-1999;	99US-0156366.
PR	01-JUL-1999;	99US-0142154.	PR	04-OCT-1999;	99US-0157117.
PR	02-JUL-1999;	99US-0142055.	PR	05-OCT-1999;	99US-0157753.
PR	06-JUL-1999;	99US-0142390.	PR	06-OCT-1999;	99US-0157855.
PR	08-JUL-1999;	99US-0142803.	PR	07-OCT-1999;	99US-0158029.
PR	09-JUL-1999;	99US-0142920.	PR	08-OCT-1999;	99US-0158232.
PR	12-JUL-1999;	99US-0142977.	PR	12-OCT-1999;	99US-0158369.
PR	13-JUL-1999;	99US-0143542.	PR	13-OCT-1999;	99US-0159293.
PR	14-JUL-1999;	99US-0143624.	PR	13-OCT-1999;	99US-0159294.
PR	15-JUL-1999;	99US-0144005.			99US-0159295.
PR	16-JUL-1999;	99US-0144085.			
PR	16-JUL-1999;	99US-0144086.			
PR	19-JUL-1999;	99US-0144325.			
PR	19-JUL-1999;	99US-0144331.			
PR	19-JUL-1999;	99US-0144333.			

PR	30-JUN-1999;	990US-0141287.
PR	01-JUL-1999;	990US-0141842.
PR	02-JUL-1999;	990US-0142154.
PR	06-JUL-1999;	990US-0142055.
PR	08-JUL-1999;	990US-0142390.
PR	09-JUL-1999;	990US-0142803.
PR	12-JUL-1999;	990US-0142977.
PR	13-JUL-1999;	990US-0143199.
PR	14-JUL-1999;	990US-0143624.
PR	15-JUL-1999;	990US-0144005.
PR	16-JUL-1999;	990US-0144086.
PR	17-JUL-1999;	990US-0144106.
PR	19-JUL-1999;	990US-0144325.
PR	20-JUL-1999;	990US-0144331.
PR	21-JUL-1999;	990US-0144332.
PR	22-JUL-1999;	990US-0144333.
PR	23-JUL-1999;	990US-0144334.
PR	24-JUL-1999;	990US-0144335.
PR	25-JUL-1999;	990US-0144352.
PR	26-JUL-1999;	990US-01445085.
PR	27-JUL-1999;	990US-01445087.
PR	28-JUL-1999;	990US-01445089.
PR	29-JUL-1999;	990US-01445192.
PR	30-JUL-1999;	990US-01445145.
PR	31-JUL-1999;	990US-01445218.
PR	23-JUL-1999;	990US-0145224.
PR	24-JUL-1999;	990US-0145226.
PR	25-JUL-1999;	990US-0145913.
PR	26-JUL-1999;	990US-0145918.
PR	27-JUL-1999;	990US-0145919.
PR	28-JUL-1999;	990US-0145951.
PR	02-AUG-1999;	990US-0146386.
PR	02-AUG-1999;	990US-0146388.
PR	03-AUG-1999;	990US-0146389.
PR	03-AUG-1999;	990US-0147038.
PR	04-AUG-1999;	990US-0147204.
PR	05-AUG-1999;	990US-0147302.
PR	06-AUG-1999;	990US-0147260.
PR	07-AUG-1999;	990US-0147303.
PR	08-AUG-1999;	990US-0147416.
PR	09-AUG-1999;	990US-0147493.
PR	10-AUG-1999;	990US-0147935.
PR	11-AUG-1999;	990US-0148171.
PR	12-AUG-1999;	990US-0148319.
PR	13-AUG-1999;	990US-0148341.
PR	13-AUG-1999;	990US-0148565.
PR	16-AUG-1999;	990US-0149368.
PR	17-AUG-1999;	990US-0149175.
PR	18-AUG-1999;	990US-0149426.
PR	20-AUG-1999;	990US-0149722.
PR	20-AUG-1999;	990US-0149723.
PR	21-AUG-1999;	990US-0149929.
PR	23-AUG-1999;	990US-0149902.
PR	23-AUG-1999;	990US-0149930.
PR	25-AUG-1999;	990US-0150566.
PR	26-AUG-1999;	990US-0150884.
PR	27-AUG-1999;	990US-0151065.
PR	27-AUG-1999;	990US-0151066.
PR	27-AUG-1999;	990US-0151080.
PR	30-AUG-1999;	990US-0151303.
PR	01-SEP-1999;	990US-0151438.
PR	01-SEP-1999;	990US-0151930.
PR	07-SEP-1999;	990US-0152363.
PR	10-SEP-1999;	990US-0153070.
PR	13-SEP-1999;	990US-0153758.

Db 389 LTVLTLIEVEKRRARAATVDEMDAFLMAVRPLPLPSKE 426

Db 371 ECIVLQEFVSAYOERRSKYDQVVEKFMPKPHKLVF 406

RESULT 15

AAB6931
ID AAB6931 standard; Protein: 424 AA.

XX AC AAB6931;

XX DT 12-APR-2001 (first entry)

XX DE Tryptophanyl-tRNA synthetase.

XX KW Tryptophanyl-tRNA synthetase; enzyme.

XX OS Candida albicans.

XX PN US6174713-B1.

XX XX PD 16-JAN-2001.

XX XX PR 16-JUN-1997; 97US-0876885.

XX PR 16-JUN-1997; 97US-0876885.

XX PA (CUBI-) CUBIST PHARM INC.

XX PI Shen X, Houman F;

XX DR WPI; 2001-201806/20.

XX DR N-PSDB; AAF55855.

XX PT New nucleic acids encoding Candida cytoplasmic tryptophanyl-tRNA

PT (tRNA) synthetases, useful for producing recombinant tRNA synthetases

PT and detecting inhibitor of Candida tRNA synthetase function

XX CC cRNA synthetases and detecting inhibitors of tRNA synthetase.

XX PS Claim 4; FIG 1; 32pp; English.

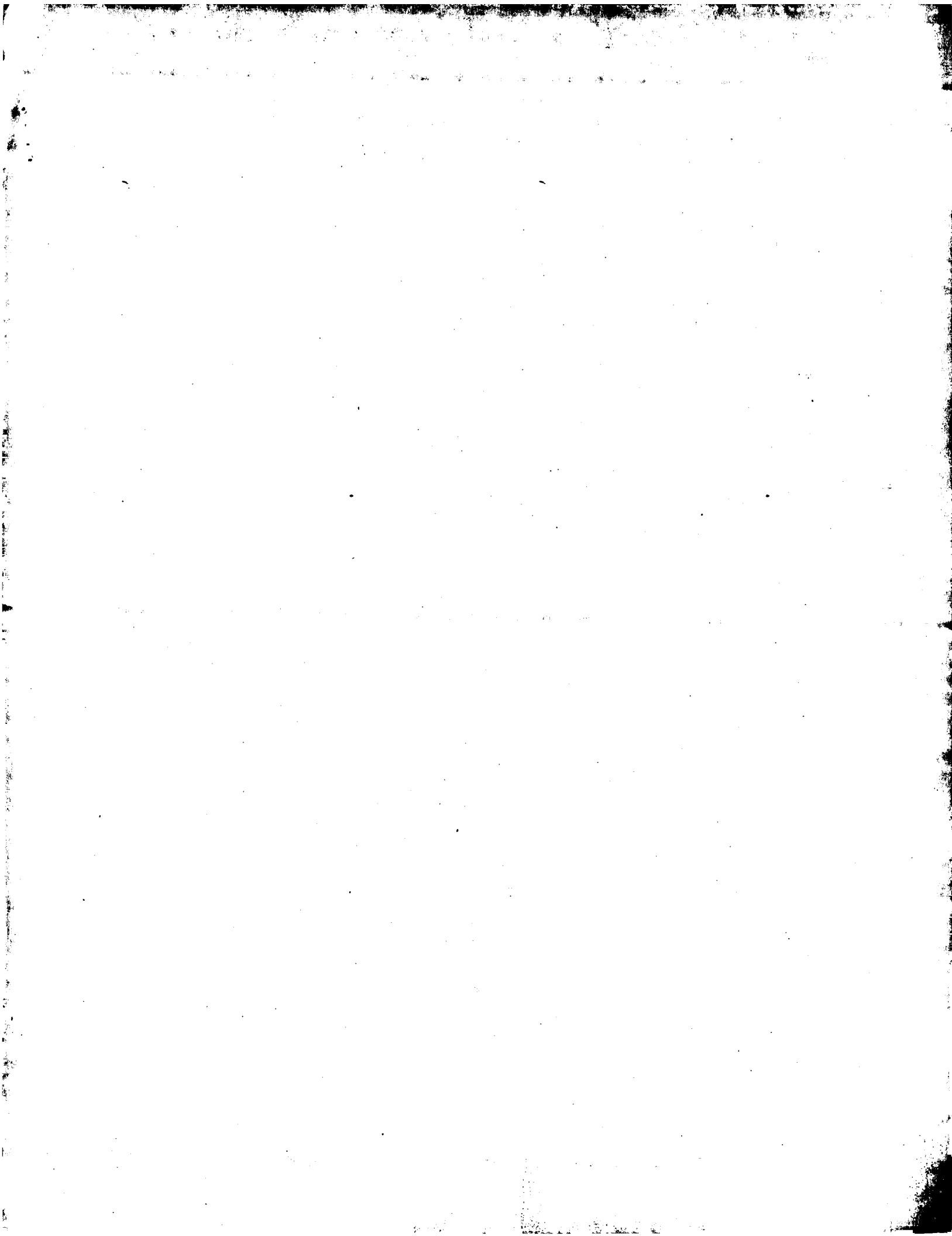
XX CC The present sequence is Candida albicans cytoplasmic tryptophanyl-tRNA

CC (tRNA) synthetase, tRNA synthetase is useful for producing recombinant

CC tRNA synthetases and detecting inhibitors of tRNA synthetase.

XX SQ Sequence 424 AA;

Query Match 54.3%; Score 1218.5; DB 22; Length 424;
Best Local Similarity 57.1%; Pwd. No. 3; 3e-16; 3;
Matches 226; Conservative 71; Mismatches 92; Indels 7; Gaps 3;
Qy 31 TBAEDEDVDPWVQ---TSSAKGIDYDKUVRFGSSKIDKELINKRERATCQRPHFIR 86
Db 13 TEESEOKITPWPWEGAVWDGKSMGNGIDKLTSQFGTKHITERPLPKQVNGEERPHFLK 72
Qy 87 RGLFFSHRDMDNQVDAVENKKPFYLTYGRGPSEAMEVGHLTPPFIPTKWLQDVENVPLVI 146
Db 73 RGVFFSQRDLDDILDLYEHGERFFLYVORGPSDSMILGHMVPFFIFIKWLOEVFDVPLVI 132
Qy 147 QMTDDEKYLWK-DLTLDQAYSGAVENAKDTIAGFDINKTRFSIDYGMNSSGFYKNVV 205
Db 133 ELLTDEKEFLFKQHQLTIDVKGAENAKDIAVGFNPENTPFLSDIQYMG--GAFYENV 190
Qy 206 KIQKHYTFNQVKGIGFTGPDQGKSPAOQAPSNSNPQIFRDTQDQCLPCAI 265
Db 191 RRSROTITSTAKAVGFPIDTSDCIGKHPASIOQIATAPSSFPDVGLSLPPKTCPLCPAID 250
Qy 266 QDPYFRMTRDVAAPRIGFPKPALLHSTPPALQQAQIKMSASDPNSSIPLTTAKQIKV 325
Db 251 QDPYFRMTRDVAADKLRTKPAJLHAKFPALQGASTMSASDTSIFMGQTAKQIQQKKI 310
Qy 326 NHKAIFSGGRDTTEBHRQGNGCDVDVSFMWLTTFLEDDDKUOBIRKDVTSGAMLTGBLK 385
Db 311 NYVAFSGGRATEEHEBELGGNFEVDVAFQYLSPPFSYDEKLAQLEOGYRKGEILSGEMKK 370
Qy 386 ALIEVLOQPLIAHQARRKEVTDIBVKEFMTPRKLNF 421



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OM protein - protein search, using sw model

Run on: July 10, 2003, 12:29:05 ; Search time 12.8495 Seconds

Perfect score: 2246

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/podata/1/iaa/5B_COMB_pep:*

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4: /cgn2_6/podata/1/iaa/6B_COMB_pep:*

5: /cgn2_6/podata/1/iaa/PCTUS_COMB_pep:*

6: /cgn2_6/podata/1/iaa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-08-876-885-26
Sequence 26, Application US/08876885
Patent No. 6174713

GENERAL INFORMATION:

APPLICANT: Shen, Xiaoyu
TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-tRNA
TITLE OF INVENTION: SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,885
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
SEQUENCE/DOCKET NUMBER: CPI-97-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-5540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear

ALIGNMENTS

Query Match 54.3%; Score 1218.5; DB 4; Length 424;
Best Local Similarity 57.1%; Pred. No. 6.0e-127;
Matches 226; Conservative 71; Mismatches 92; Indels 7; Gaps 3;

QY	31 TEAEEDFVDDWTVO---TSSAGKGDYDKLIVRFGSSKIDKELNRIERATGRRPHFLR
Db	13 TEESOKITPWEVEGAVIDGSKMGIDYDKLISQFGTKHTEETLERPKVOTGEEBPHFLK 72

QY 87 RGTFSSHRDMNQVLDAYENKKPFVLYTGRGPSSSAMVHGLIPPTFKWILQDVNNPLVLT 146
Db 73 RGWFPSQRDLDRDILYVERGEPEPFLITGRGPSSSMHGLIPPTFKWILQDVNNPLVLT 132
QY 147 QMDDEKYLW-DLTDORGYGDAVENAKOIIACAFRDINKTPFEDDLYGMSSGFYKNTV 205
Db 133 ELTDDKEFLKHOQTIDDVKGFAANAKOIIAVERNPENTIFSDLQMG--GAFFYNTV 190
QY 206 KIQKHVNQVKGIGFMDCTGKISPAIQAAPSNSPQIQRDRDPCIAID 265
Db 191 RTSRQQTSTAKAVFGFTSDCIGKIHAFSIOATTAFFSPSPDVLGLPPKTCIPLCAID 250
QY 266 QDPYFRMTRDVAEPRIGKPALLHSTFPALQAGAQTKNSASDPNSIFLDTAKQIKTV 325
Db 251 QDPYFRMTRDVAEPRIGKPALLHSTFPALQAGAQTKNSASDPNSIFLDTAKQIKTV 310
QY 326 NKRAFSGERDTBFRHROFGNCVDVSFMLTEFLDDKLEQIRKDYSGAMLTGELKK 385
Db 311 NKYAFSGGATABERBLRELGPNPEVDAFOQLSFSSYDDEKLQAQEQYRGEELISGEMKK 370
QY 386 ALIEVLQPLAEHQARKEVDEWKEFMPRKLSF 421
Db 371 ECTIVLQEFVSAQERRSKVDPQTEKENKPKHLVP 406

RESULT 2
US-08-928-100-2
; Sequence 2, Application US/08928100
; Patent No. 6046174
; GENERAL INFORMATION:
; APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6046174el trps
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928.100
FILING DATE: 12-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gianni, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE DOCKET NUMBER: P31624-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match: Best local Similarity: 8.3%; Score: 185.5; DB: 3; Length: 341;

Matches: 81; conservative: 60; mismatches: 128; Indels: 69; Gaps: 15;
QY 107 KPPVLYTGGRPSEAMVHGLIPPTFKWILQDVNNPLVLTQMTDKY-LWKDLTLQAY 165
Db 3 KPIIL-TGDRPTGK-LHGHVGSLNR-----VLLQEEBDKYDWMVFLLADQAL 49
QY 166 GDAVEN-----AKDIIACGFDFNKTFIF--SDLDYGMMSGFYKNNW--KIQK 209
Db 50 TDHAKDPQTIVESIGNVALDYAVGLDPMKNTQSQFELAELSMYMMVLSLAR 109
QY 210 HVTFENQVKGIGFMDCTGKISPAIQA--PSFSNSPQIQRDRDPCIAID 267
Db 110 NPTVKTBISOKGGESIPTGFLVYTAQAMDTARKANY----VPGTDQK 156
QY 268 PYFRMTRD----VARIGPKALLHSTFPALQAGAQTKNSASDPNSIF 313
Db 157 PMIEQTRTYRSFENNAYNCNDVLUVEPEGIYPNE--RAGRFLGLDG-NAKWSKS-LNNGIY 212
QY 314 ITDTAKQIKTVNKHAPSGGRDTBFRHROFGNCVDVSFMLTEFLDDKLEQIRK 371
Db 213 LADDATURKUMSMYTDPHIRVEDPGKIEGN--MVFTYLDVGRPRDAQEITADMKE 268
QY 372 DYTSGAMLTCRHLKALIEVQIOPLAEHQARKEVDEI 409
Db 269 RYQRGEGIGDVTKRVLLEIIRLEGPIREBRIEFAKDM 306

RESULT 3
US-09-492-581-2
; Sequence 2, Application US/09492581
; Patent No. 6346409
; GENERAL INFORMATION:
; APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6346409el trps
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,581
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928.100
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gianni, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE DOCKET NUMBER: P31624-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; US-08-743-130A-39

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.3%; Score 164.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 1.6e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

RESULT 6
US-08-743-130A-2
; Sequence 2, Application US/08743130A
; Patient No. 581987

GENERAL INFORMATION:

APPLICANT: Sasanfar, Mandana
APPLICANT: Gallant, Paul L.
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Jianhui
APPLICANT: Houman, Fariba

TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743-130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brock Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI95-12
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 861-6240
; FAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-743-130A-2

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

Query Match 7.2%; Score 162.5; DB 2; Length 409;

Best Local Similarity 20.7%; Pred. No. 2.7e-09; Mismatches 132; Indels 107; Gaps 16;

Matches 78; Conservative 59;

RESULT 7
US-08-705-868-4
; Sequence 4, Application US/08705868
; Patient No. 581987

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Coleman, Roger

APPLICANT: Au-Young, Janice

APPLICANT: Murty, Lynn E.

TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/05,868

FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

us-09-813-718-10_copy_48_471.rain

NAME: Gimmi, Edward R
 REGISTRATION NUMBER: 38 891
 REFERENCE DOCKET NUMBER: P31624
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEX: 610-270-5090
 ;
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ;
 US-08-923-867-2
 Query Match 4.8%; Score 108; DB 2; Length 197;
 Best Local Similarity 25.3%; Pred. No. 0.00092; Mismatches 73; Indels 24; Gaps 6;
 Matches 42; Conservative 27; Mismatches 73; Indels 24; Gaps 6;
 Db
 Qy 306 SDPNSSIFLTDAKQIKTKWNHAFSGGRDTIEHRQPGNCVDSMLITF--LEDD 363
 260 IPCAIDODPYFRMTRD-----VAPRIGYKPALHSTFPALQAGOTKMSA 305
 5 VPVGTDQKPMIEQTREIVRSFNNAYNCNDVLVEPEGIYPENE--RAGRLLGLDG-NAKMSK 61
 Db
 Qy 364 DKLQIRQKTYTSGAMLTGELKKALIEVTOPLIAHQARKEVTDBI 409
 117 QEIADMKERYQRGGLGDVKTKRYLLEILRELGPIRERRIEFAKDM 162
 Db
 Qy 364 DKLQIRQKTYTSGAMLTGELKKALIEVTOPLIAHQARKEVTDBI 409
 117 QEIADMKERYQRGGLGDVKTKRYLLEILRELGPIRERRIEFAKDM 162
 RESULT 12
 US-08-928-100-4
 Sequence 4, Application US/08928100
 ; Patent No. 6046174
 GENERAL INFORMATION:
 APPLICANT: Gentry, Danile
 APPLICANT: Greenwood, Claire
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: No. 6046174el trps
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0339
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/183,134
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/923,867
 FILING DATE: 04-SEP-1997
 APPLICATION NUMBER: 9619072.3
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimmi, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE DOCKET NUMBER: P31624
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ;
 US-08-928-100-4
 Query Match 4.8%; Score 108; DB 4; Length 197;
 Best Local Similarity 25.3%; Pred. No. 0.00092; Mismatches 73; Indels 24; Gaps 6;
 Matches 42; Conservative 27; Mismatches 73; Indels 24; Gaps 6;

OM protein - protein search, using sw model	
Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.6
Run on: July 10, 2003, 12:28:00 ; Search time 16.4461 Seconds	(without alignments)
Sequence: 1 MSYKAAGEDDYKADCPPGPNP.....VTDIEIVKEMTPRKLSPDFQ 424	2478.466 Million cell updates/sec
Scoring table: BLOSUM62	
Searched: Gapop 10.0 , Gapext 0.5	
Total number of hits satisfying chosen parameters: 283224	
Minimum DB seq length: 0	
Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0%	
Listing first 45 summaries	
Database : PIR_73.*	
1: pirl:*	
2: pir2:*	
3: pir3:*	
4: pir4:*	
Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Query Match Length DB ID
1	A41706 tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
2	tryptophanyl-tRNA synthetase; Homo sapiens (man)
3	C;Species: Homo sapiens (man)
4	C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 03-Jun-2002
5	C;Accession: A41633; A41706; S19246; JN0676; JH0533; S26287
6	R;Fleckner, J.; Rasmussen, H. H.; Justesen, J.
7	Proc. Natl. Acad. Sci. U.S.A., 88, 11520-11524, 1991
8	A;Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma
9	A;Reference number: A41633; MUID:92107982; PMID:1763065
10	A;Status: Preliminary
11	A;Molecule type: mRNA
12	A;Cross-references: GB:X59892; NID:930820; PIDN:CAA42545.1; PID:930821
13	R;Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.
14	J. Biol. Chem. 266, 24245-24248, 1991
15	A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.
16	A;Reference number: A41706; MUID:92105071; PMID:1761529
17	A;Accession: A41706
18	A;Status: Preliminary
19	A;Molecule type: mRNA
20	A;Residues: 1-471 <RUB>
21	A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:9184657
22	R;Buwitt, U.; Flohr, T.; Boettger, E.C.
23	EMBL J. 11, 489-500, 1992
24	A;Title: Molecular cloning and characterization of an interferon induced human cDNA with hypothetical prote
25	A;Reference number: S19246; MUID:92164636; PMID:1537332
26	A;Accession: S19246
27	A;Status: Preliminary
28	A;Molecule type: mRNA
29	A;Residues: 1-71 <RLE>
30	A;Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA4450.1; PID:932709
31	A;Note: 213-Ser and 214-Tyr were also found
32	R;Frolova, L.Y.; Grigorieva, A.Y.; Sudomina, M.A.; Kisseelev, L.I.
33	Gen 128, 237-245, 1993
34	A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response element
35	A;Reference number: JN0676; MUID:93292992; PMID:7685728
36	A;Accession: JN0676
37	A;Molecule type: DNA
38	A;Residues: 1-141;162-471 <FROI>
39	A;Cross-references: GB:X67918; GB:S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; NID:g37974; GB:X67925; GB:S62855; NID:g37975; GB:X67926; GB:S62856; NID:g37976; GB:X67927
40	A;Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 34
41	A;Note: this translation is not annotated in Genbank entries HSRSX1A, HSRSX1B, HSRSX2.
42	R;Frolova, L.Y.; Sudomina, M.A.; Grigorieva, A.Y.; Zinovieva, O.L.; Kisseelev, L.I.
43	Gene 109, 2911-2916, 1991
44	A;Title: Cloning and nucleotide sequence of the structural gene encoding for human tryptic
45	A;Reference number: JH0533; MUID:92112058; PMID:1765274
46	A;Accession: JH0533
47	A;Molecule type: mRNA

A;Residues: 1-212, 'GD', 215-471 <PRO>
A;Cross-references: GB:M61715; NID:9340367; PID:AAA61298.1; PID:9340368
A;Experimental source: fibroblast
C;Genetics:
A;Gene: GDB:WARS; ITP53
A;Map position: 14q23-14q31
A;Introns: 33/3; 105/1; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
C;Superfamily: mammalian tryptophanyl-tRNA synthetase; ATP; ligase; protein biosynthesis
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;19-64/Domain: amino acid-tRNA ligase repeat homology <ATL>

Query Match 99.3%; Score 2231; DB 1; Length 471;
Best local Similarity 99.5%; Pred. No. 1.8e-173; Mismatches 0; Indels 0; Gaps 0;
Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYKAAGEDDYKACDCCPGNAPTSNHNHGPDATEABEDFYDWPWTQTSAAKGIDYDKLTIVRF 60
Db 48 MSYKAAGEDDYKACDCCPGNAPTSNHNHGPDATEABEDFYDWPWTQTSAAKGIDYDKLTIVRF 107
QY 61 GSSKIDKEILNRRTRATGCRPHFLRGIFPSRDRMNDQVTDAYENKKPYLYTGRGSSE 120
Db 108 GSSKIDKEILNRRTRATGCRPHFLRGIFPSRDRMNDQVTDAYENKKPYLYTGRGSSE 167

QY 121 AMVGHLLPPIFTKWLQDVNVPLVIQMDDEKYLWKLDTDOAYGDAVENAKDIACGF 180
Db 168 AMVGHLLPPIFTKWLQDVNVPLVIQMDDEKYLWKLDTDOAYGDAVENAKDIACGF 227

QY 181 DINKFIFISDLDDNGMSSGFYKVNVKIQRKVTNQVKGIFTGFTDSDCIGKIFPAIQAP 240
Db 228 DINKFIFISDLDDNGMSSGFYKVNVKIQRKVTNQVKGIFTGFTDSDCIGKIFPAIQAP 287

QY 241 SFNSNPQFPRDFDIQCLIPCAIDQDPYFRMRDVAARRIGPKPALHSTFPALQAO 300
Db 288 SFNSNPQFPRDFDIQCLIPCAIDQDPYFRMRDVAARRIGPKPALHSTFPALQAO 347

QY 301 TKSASDENSIILTDTAQIKTKVKNKAFASGRDTEBHRQGGNCVDVSMYLTPFL 360
Db 348 TKSASDENSIILTDTAQIKTKVKNKAFASGRDTEBHRQGGNCVDVSMYLTPFL 407

QY 361 DDDKLEQIRKDVTSGAMLTGEKLKKALIEVLQPLIAEHQARRKEVTDIVKEMTPKLS 420
Db 408 EDDKLEQIRKDVTSGAMLTGEKLKKALIEVLQPLIAEHQARRKEVTDIVKEMTPKLS 467

QY 421 DFQ 424
Db 468 FDFQ 471

RESULT 2

YBBO
tryptophanyl-tRNA ligase (EC 6.1.1.2) [validated] - bovine
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 03-Jun-2002
C;Accession: A40279; JN0354; S10460; S14540
R;Garrett, M.; Paolet, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gendar, J.C.; Benedicto, A.; Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic s
A;Reference number: A40279; MUID:9132348; PMID:1907847
A;Accession: A40279
A;Molecule type: mRNA
A;Residues: 1-475 <GAR>
A;Cross-references: GB:M74074; EMBL:X533918; NID:9163798; PID:AAA30799.1; PID:9163799
A;Experimental source: pancreas
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
R;Zarganova, T.A.; Kovalova, G.K.; Favorova, O.O.; Revina, H.B.; Relezinskaya, I.H.
Biorg. Khim. 15, 1307-1311, 1989
A;Title: Amino acid sequence of several peptides of tryptophanyl-tRNA synthetase from ca
A;Reference number: JN0354; MUID:90211408; PMID:2631684
A;Accession: JN0354
A;Molecule type: protein

RESULT 3

YRBPR
tryptophanyl-tRNA ligase (EC 6.1.1.2) [validated] - rabbit

N;Alternate name: tryptophanyl-tRNA synthetase

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1992 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002

C;Accession: A33904; S37396

R;Lee, C.C.; Craigie, W.J.; Munay, D.M.; Harlow, E.; Caskey, C.T.
Proc. Natl. Acad. Sci. U.S.A. 87, 3508-3512, 1990
A;Title: Cloning and expression of a mammalian peptide chain release factor with sequence A;Reference number: A33904; MUID:90239043; PMID:2185472
A;Accession: A35504
A;Molecule type: mRNA
A;Residues: 1-475 <LR>
A;Cross-references: GB:M33460
R;Prolova, L.Y.; Dolphin, M.E.; Justesen, J.; Powell, R.J.; Drudgeon, G.; McCaughan, K.K.; EMBJ. 12, 4013-4019, 1993
A;Title: Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are A;Reference number: S37396; MUID:94009008; PMID:8404867
A;Molecule type: mRNA
A;Residues: 166-177 <PRO>
C;Genetics:
A;Gene: WRS
C;Complex: homodimer [validated, MUID:94009008]
C;Function:
A;Description: EC 6.1.1.2 [validated, MUID:94009008]; catalyzes the ATP-dependent formation of a peptide chain release factor and tryptophanyl-tRNA synthetase
A;Note: mammalian WRS (tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homology

C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; metalloprotein; protein F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL> F;174-177/Region: ATP-binding motif (HKG)

Query Match Local Similarity 90.9%; Score 2041; DB 1; Length 475; Matches 380; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

Best Local Similarity 89.8%; Pred. No. 5; le-158;

Matches 380; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

Query 2 SYKAAGEDYKDCPPGNPAPTSNHPDPAEEDFVDPWTQTSAAKGIDYKLVREG 61

Db 53 SYKEAMGEDYKDCPPGNSTPSHGDEAVIDDKEDFDVDPWTWRTSSAKGIDYKLVQFG 112

Query Match Local Similarity 90.5%; Score 2032; DB 2; Length 431;

Matches 380; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Best Local Similarity 89.6%; Pred. No. 2.8e-157;

Matches 380; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Query 62 SSKIDKLLEINRERATGQRPHFLRGIFFSHGRDMQVLDAYENKKPFYLTYGRGSE 121

Db 113 SSKIDKLLEINRERATGQRPHFLRGIFFSHGRDMQVLDAYENKKPFYLTYGRGSE 172

Query 122 MIVGHLIPFIFTKWLQDVFNVLVQIOMTDKLTQDQYGAVIDENAKDIIAGFD 181

Db 173 MIVGHLIPFIFTKWLQDVFNVLVQIOMTDKLTQDQYGAVIDENAKDIIAGFD 232

Query 182 IKTKEFSDLQMGMSGFVKWVQKQHVTPNQVKGIFGFTSDTIGKISFPQIAQAPS 241

Db 233 VNKTFIFPSDLYNGMSGPYKVNVKQIKHVTENQVKQIFGFTSDCIGKISFPQIAQAPS 292

Query 242 FSNSFQIFRDRDIOCLIPCAIDQDPYFRMRDVAPRIGYPKALLHSFFPALQDAQT 301

Db 293 FSNSFQIFHGGQADICLICPAIDQDPYFRMRDVAPRIGYPKALLHSFFPALQDAQT 352

Query 302 KNSASDNNSTELTDATAKQIKTKVNKHAFSGGRDTBEHRQGGNCDDVVFMMYLTFFL 361

Db 353 KNSASDNNSTELTDATAKQIKTKVNKHAFSGGRDTBEHRQGGNCDDVVFMMYLTFFL 412

Query 362 DDKLQLQIRKQYTGSGMLTGKELKKALIEVLOPLIAHQARKEVTDIYKEFMTPKLSF 421

Db 413 DDKLQLQIRKQYTGSGMLTGKELKKALIEVLOPLIAHQARKEVTDIYKEFMTPKLSF 472

Query 422 DFFQ 424

Db 473 HQ 475

RESULT 4

S50053 tryptophan-tRNA ligase (EC 6.1.1.2) alpha-2 chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002

C;Accession: S50053; S50052; MUID: 95018226; PMID: 932716

A;Accession: S50053; S50052; MUID: 95018226; PMID: 932716

A;Molecule type: mRNA

A;Residues: 1-481; T88561

A;Cross-references: EMBL:X69657; NID:955437; PIDN:CAA49348.1; PID:955438

A;Genetics: LSF

A;Note: intron position was determined by sequencing of genomic DNA

A;Accession: S50052

A;Molecule type: mRNA

A;Residues: 1-475 <PRW>

A;Cross-references: EMBL:X69656; NID:955435; PIDN:CAA49347.1; PID:955436

A;Genetics: SSF

A;Status: preliminary; translated from GB/EMBL/DDJB

R;Kiselev, L.I.

Biochem 75, 1027-1039, 1993

A;Title: Mammalian tryptophanyl-tRNA synthetases.

A;Reference number: 149391; MUID: 9457759; PMID: 7715282

A;Accession: 149391

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-395 <GB2>

A;Cross-references: EMBL:Z50142; PIDN:CAA90500.1; GSDB:GN00066; SPDB:SPAC2F7.13C

A;Experimental source: strain 972h-; cosmid c2f7

C;Genetics: <JSP>

A;Gene: WRS

A;Introns: 475/2
A;Note: the 11st of introns may be incomplete; clone w13
C;Genetics: <SSF>
A;Gene: WRS
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: alternative splicing; aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicted
F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted
F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>

Query Match Local Similarity 90.5%; Score 2032; DB 2; Length 431;

Matches 380; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Best Local Similarity 89.6%; Pred. No. 2.8e-157;

Matches 380; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Query 1 MSYKAAGEDYKADCPGPGNPAPTSNHGPDATEAEEDFVDPWTQTSAAKGIDYKLVRF 60

Db 52 MSYKAAGEDYKAGCPGPGNPAPTSNHGPDATEAEEDFVDPWTQTSAAKGIDYKLVRF 111

Query 61 GSSKDKEKLLEINRERATGQRPHFLRGIFFSHGRDMQVLDAYENKKPFYLTYGRGSE 120

Db 112 GSSKDKEKLLEINRERATGQRPHFLRGIFFSHGRDMQVLDAYENKKPFYLTYGRGSE 171

Query 121 AMVHGHLIPFIFTKWLQDVFNVLVQIOMTDKLTQDQYGAVIDENAKDIIAGF 180

Db 172 AMVHGHLIPFIFTKWLQDVFNVLVQIOMTDKLTQDQYGAVIDENAKDIIAGF 231

Query 181 DINKPFIISDLYNGMSGPYKVNVKQIKHVTENQVKQFGFTSDCIGKISFPQIAQAP 240

Db 232 DINKPFIISDLYNGMSGPYKVNVKQIKHVTENQVKQFGFTSDCIGKISFPQIAQAP 291

Query 241 SFNSNPQIFRDRDIOCLIPCAIDQDPYFRMRDVAPRIGYPKALLHSFFPALQDAQT 300

Db 292 SFNSNPQIFRDRDIOCLIPCAIDQDPYFRMRDVAPRIGYPKALLHSFFPALQDAQT 351

Query 301 TKMSASDPNNSIELTDATAKQIKTKVNKHAFSGGRDTBEHRQGGNCDDVVFMMYLTFFL 360

Db 352 TKMSASDPNNSIELTDATAKQIKTKVNKHAFSGGRDTBEHRQGGNCDDVVFMMYLTFFL 411

Query 361 EDDDKLQLQIRKQYTGSGMLTGKELKKALIEVLOPLIAHQARKEVTDIYKEFMTPKJS 420

Db 412 EDDDKLQLQIRKQYTGSGMLTGKELKKALIEVLOPLIAHQARKEVTDIYKEFMTPKJS 471

RESULT 5

S58157 hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Dec-1999

C;Accession: S58157; T88561

R;Gentles, S.; Churcher, C.M.

Submitted to the EMBL Data Library, July 1995

A;Reference number: S58145

A;Accession: S58157

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <GEN>

A;Cross-references: EMBL:Z50142; NID:9105283; PIDN:CAA90500.1; PID:91052796

R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

Submitted to the EMBL Data Library, July 1995

A;Reference number: Z21799

A;Accession: T38561

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-395 <GB2>

A;Cross-references: EMBL:Z50142; PIDN:CAA90500.1; GSDB:GN00066; SPDB:SPAC2F7.13C

A;Experimental source: strain 972h-; cosmid c2f7

C;Genetics: SPDB:SPAC2F7.13C

A;Gene: SPDB:SPAC2F7.13C

A; Map position: 1
C; Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 53.9%; Score 1210; DB 2; Length 395;
Best Local Similarity 59.6%; Pred. No. 1.1e-90; Mismatches 91; Indels 8; Gaps 4;

Matches 235; Conservative 60; Mismatches 91; Indels 8; Gaps 4;

Oy 34 EEDPFDWPWVOTV---SAKGIDYDKLIVRGSSKIDELINRIERATGQRPHFLRGI 89
Db 4 BEQIVTPWDVKGSIVDGERKIDYERLTQFGTRKITPBOLERPEKLITGKKPHLLRGA 63

Oy 90 FSHDRDMNOVLDAYENKPKFYLTGRGSSSEAMEVGHJPFITKMLQDVNPVLWT 149
Db 64 FSHDRDFMILDYRDYEQKPKFYLTGRGSSPSSDMHLGHMIPFMFCWKWLQDVNPVLWT 123

Oy 150 DEREKILWKD-LTLDQAYGDAVENAKDIAACGPDKINKTFIFSDIDYGMSSGFYKVWIKI 208
Db 124 DDEKEFLPKGQSYLSDCQFARENNAKDLAVGFDKKTETPMNSTYG-GAFYQNVRIA 181

Oy 209 KHYTFNQVKIGFDTSPCGKTSFPATOAARSNSNSPQIFRDRDIOCLPCAIODP 268
Db 182 KCTIANOSKACFGFTDSDSIGKIHFASTOAPSPSSSFPHIFNGAKDIPCLPCAIODP 241

Oy 269 YFIRNTDYVAAPRIGPKPAHLHSTFPALQAGTOMSADDPNNSIFLTQAKQTKWNKH 328
Db 242 YFRLTLDYSGRLKFKPKPALHHSRFPPALQGPQSKMSASKDSALFMTDTPKTKNKH 301

Oy 329 AFSGGRDTIEEHRQFGNCDVDSFMLTFPLEDDKLEQIRKDYTGAMLTGELKKALI 388
Db 302 AFSGGATTEIHRKGKGPDVAYQYISFFLPDDEKKQKLMNTYKACTLSGEMKRCI 361

Oy 389 EVIQPLIAEHQARKEVTDIEVKEFMT-PRKLSF 421
Db 362 KLUQQFVSDFOAARRSKVUDATLDMFMDSRKLEN 395

RESULT 6

551901 TRYPTOPHAN-tRNA ligase (EC 6.1.1.2) [similarity] - Yeast (*Saccharomyces cerevisiae*)
N; Alternative names: protein HRE42; protein 00712; tryptophanyl-tRNA synthetase
C; Species: *Saccharomyces cerevisiae*
C; Date: 05-May-1995 #sequence revision 03-Aug-1995 #text_change 03-Jun-2002

C; Accession: S51901; S59177; S66793
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
R; Submitted to the EMBL Data Library, January 1995

A; Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including a Delta and a Delta.

A; Reference number: S51848

A; Accession: S51901
A; Molecule type: DNA
A; Residues: 1-432 <VAN>
A; Cross-references: EMBL:Z48149; NID:9663234; PIDN:CAA8164.1; PID:9663256
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995

A; Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the delta element.

A; Reference number: S59156; MUID:96076631; PMID:7502582

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
A; Residues: 1-432 <VAN>
A; Cross-references: EMBL:Z48149; NID:9663234; PIDN:CAA8164.1; PID:9663256
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R; Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
R; Submitted to the Protein Sequence Database, July 1996

A; Reference number: S66791
A; Accession: S66793
A; Molecule type: DNA
A; Residues: 1-432 <DUR>
A; Cross-references: EMBL:Z74839; NID:91419947; PIDN:CAA99110.1; PID:91419948; GSPDB:GN00
A; Experimental source: strain S288C
C; Genetics:
C; Genetics:

A; Gene: SGD:WRS1; WRS1; MIPS:YOL097c

A; Cross-references: SGD:S0005457
A; Map position: 15L
C; Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 51.8%; Score 1163; DB 2; Length 432;
Best Local Similarity 54.8%; Pred. No. 1.1e-86; Mismatches 217; Indels 8; Gaps 3;
Matches 217; Conservative 71; Mismatches 100; Indels 8; Gaps 3;

F;117-120/Region: ATP-binding motif (HXGH)

Oy 30 ATAEEDPFDWPWV---QNSAKGIDYDKLIVRGSSKIDELINRIERATGQRPHF 84
Db 19 STDVKEQVTPMDVEGGVDEOGKAQNDYDKLQKETKPVNEETLKRKFQVTPGEPHF 78

Oy 85 LRGIGFSSHRSRNQVLDAYENKPKFYLTGRGSSSEAMWGHLIPFIFTKQLODVNPVL 144
Db 79 LRGIGFSSHRSRNQVLDAYENKPKFYLTGRGSSPSSDMHLGHMIPFMVFTKMLQEVFDVPL 138

Oy 145 VIQMTDDEKYLWK-DLTIDQAYGDAVENAKDIAACGFDINKTFIFSDIDYGMSSGFYKN 203
Db 139 VIELTDBEKFELKHKLNUINDVNKFARENNAKDTIAVGRPDKNTFISDLOYNG-GAFYET 196

Oy 204 VKVKQKHTFNQVKIGFEGFTSDCIGKISFPALQAAPSFSNSFPQIFRRDRDIOCLJPCA 263
Db 197 VRVSRQITGTSKAVKIGFENDSDCIGKHEFASIQIAFPSSFPNVLGILPDKTPCIPCA 256

Oy 264 IDDPYFMRTRVAYAPRIGPKALLISTFPLOGAQTMASDPNNSIFLTDATOKIT 323
Db 257 IDDPYFVRVCDWADKLUKYSKPDLHHSRFPPALQGSTKMSASDDTTAIFWDTPKQIK 316

Oy 324 KUNKGHTSGGRTIEBHQFGNCNDVDSFMLTFPLEDDKLEQIRKDYTGAMLTGEL 383
Db 317 KUNKGHTSGGRTIEBHQFGNCNDVDSFMLTFPLEDDKLEQIRKDYTGAMLTGEL 376

Oy 384 KQALIEVQPLTABHQARKEVTDIEVKEFMPRKL 419
Db 377 KKCIETIQLQEVKAQERRAQVDEETLDFKMPVPHKL 412

RESULT 7

C0190 TRYPTOPHANYL-tRNA synthetase (trps) [imported] - *Sulfolobus solfataricus*

C; Species: *Sulfolobus solfataricus*
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001

R; She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Yong, I.; Jeffries, A.C.; Kozena, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Garrett, R.A.; Ragan, M.A.; Seneca, C.W.; Van der Oost, J.
R; Submitted to GenBank, April 2001.

A; Description: Sulfolobus solfataricus complete genome.

A; Accession: C90190
A; Reference number: Ag9139
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-386 <KUR>
A; Cross-references: GB:AB006641; NID:gi13813608; PIDN:ANK40778.1; GSPDB:GN00155
A; Genetics:
A; Gene: trps

C; Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 40.4%; Score 907; DB 2; Length 386;
Best Local Similarity 48.6%; Pred. No. 6.2e-66; Mismatches 191; Indels 24; Gaps 10;
Matches 191; Conservative 68; Mismatches 110; Indels 24; Gaps 10;

Oy 31 TEAEEDPFDWPWVQTSSAKG-IDYDKLIVRGSSKIDELINRIERATGQRPHF 89
Db 6 TMDEPFTPWPWV---KGKVYDKLIVQGTCQKITEELKORIKNLAGDL-HVMLRNV 59

Oy 90 FSHDRDMNOVLDAYENKPKFYLTGRGSSSEAMWGHLIPFIFTKMLQDVNPVL 149
Db 60 FSHDRDFMILDYRDYEQKPKFYLTGRGSSPSSDMHLGHMIPFMVFTKMLQEVFDVPL 118

Oy 150 DDEKYLWK-DLTIDQAYGDAVENAKDIAACGFDINKTFIFSDIDYGMSSGFYKNV 208

RESULT 8

C75020 trypophanyl-tRNA synthetase (trps) PAB111 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi (strain Orsay)
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: C75020
 R;anonymous, Genoscope
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: C75020
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-385 <KAW>
 A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:GAB50601.1; PID:9545911
 A;Experimental source: strain Orsay
 A;Gene: PH1921
 C;Superfamily: yeast tyrosine-tRNA ligase
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 27.9%; Score 626.5; DB 2; Length 301;
 Best Local Similarity 44.2%; Pred. No. 2.8e-43; Matches 134; Conservative 56; Mismatches 92; Indels 21; Gaps 7;

Db 1 122 MHVGHLLPFITFKWMLQDVNVPLIVQMTDDEKYLWQD-LTLDQAYGDAVENAKDIAACF 180
 Qy 181 DMDKTFPSDLQDGMSGFYKVNWKIQHVFPNOVKGIGFTDSDCIGKSPATOP 240
 Db 61 DEPDKTFIFQNSEP---TKIYVMAIPAKKINFSMAKAVFGTEQSOKGMIFPPAQTAP 116
 Qy 241 SGSNSFQIRRTDIQILPRAIDOPYFRTRDVARIGPKPALHSTFPALOAQ 300
 Db 117 TF-----FERK--RCLIPAIQDPYWRQLQRDFAESLGYTKTAALHSKVPSLSL 166
 Qy 301 TKGASDENSSFLTDQKQTKVUNKAHFSGGRDTBEHRPGNGCDVDSWMLTFL 360
 Db 167 GRSMSASKPETAIIILSDPVEDKVKWFELTIGRPTIKBORKGGPERKCVPKWLFFF 226
 Qy 361 EDDDKLQKROY---TSGAMITGELKALISVLQPLAHEQARRKEVTDIEVKEFMPR 417
 Db 227 EDDDK- KLIKERRYACKNGEELTCGECKRYLISKIQEFLKERQRKK-AEKLVEFKYTG 283
 Qy 418 KLS 420
 Db 284 KLA 286

RESULT 9

G71206 tryptophanyl-tRNA ligase (EC 6.1.1.2) - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 03-Jun-2002
 C;Accession: G71206
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Oitoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchihara, M.; DIA Res. 5, 55-56, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: G71206
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-301 <KOW>
 A;Cross-references: GB:APP00007; NID:93236134; PIDN:BA31046.1; PID:93258363
 A;Experimental source: strain Or3
 A;Gene: PH1921
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 A;Genetics:
 C;Genetics:

Db 1 269 YERMTDVAPRIGYPKPALLHSTFPALQAGQTKMSASDPNSIILFDTAKQIKTKNKH 328
 Qy 226 YRLQDIAESLGYYKAAQHSKELPLPITGPEKSNSSNPETAVLYVDPKTVERKIMY 285
 Qy 329 AMSGGRDTEERHOFGGCNDVUSPMWLTFFEDDKLQEIRKDY--TSGAMLGTGALKALIE 387
 Db 388 IEVLQPLTAEHQARKEVTDIEVKEFMPRKL 420
 Db 346 IDKLNNELEHR-RRREAKEALVHFKDGKLA 377

RESULT 8

C75020 trypophanyl-tRNA synthetase (trps) PAB111 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi (strain Orsay)
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: C75020
 R;anonymous, Genoscope
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: C75020
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-385 <KAW>
 A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:GAB50601.1; PID:9545911
 A;Experimental source: strain Orsay
 A;Gene: PH1921
 C;Superfamily: yeast tyrosine-tRNA ligase
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 27.9%; Score 626.5; DB 2; Length 301;
 Best Local Similarity 44.2%; Pred. No. 2.8e-43; Matches 134; Conservative 56; Mismatches 92; Indels 21; Gaps 7;

Db 1 122 MHVGHLLPFITFKWMLQDVNVPLIVQMTDDEKYLWQD-LTLDQAYGDAVENAKDIAACF 180
 Qy 181 DMDKTFPSDLQDGMSGFYKVNWKIQHVFPNOVKGIGFTDSDCIGKSPATOP 240
 Db 61 DEPDKTFIFQNSEP---TKIYVMAIPAKKINFSMAKAVFGTEQSOKGMIFPPAQTAP 116
 Qy 241 SGSNSFQIRRTDIQILPRAIDOPYFRTRDVARIGPKPALHSTFPALOAQ 300
 Db 117 TF-----FERK--RCLIPAIQDPYWRQLQRDFAESLGYTKTAALHSKVPSLSL 166
 Qy 301 TKGASDENSSFLTDQKQTKVUNKAHFSGGRDTBEHRPGNGCDVDSWMLTFL 360
 Db 167 GRSMSASKPETAIIILSDPVEDKVKWFELTIGRPTIKBORKGGPERKCVPKWLFFF 226
 Qy 361 EDDDKLQKROY---TSGAMITGELKALISVLQPLAHEQARRKEVTDIEVKEFMPR 417
 Db 227 EDDDK- KLIKERRYACKNGEELTCGECKRYLISKIQEFLKERQRKK-AEKLVEFKYTG 283
 Qy 418 KLS 420
 Db 284 KLA 286

RESULT 10

G8433 tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Accession: G8433
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bequist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithäuser, B.; Keller, R.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabbal, Jung, K.H.; Alam, M.; Fritas, T.; Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A;Title: Genome sequence of Halobacterium species NRC-1
 A;Reference number: A84160; MUID:20504483; PMID:1116950
 A;Accession: G8433
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-380 <STO>
 A;Cross-references: GB:AE004437; NID:910581646; PIDN:AAC220355.1; GSPDB:GN00138
 C;Genetics:

Db 1 273 TRDVA PRIGYPKPALLHSTFPALQAGQTKMSASDPNSIILFDTAKQIKTKNKH 322
 Qy 224 QRDFAESLGYYKTAIHSKFVPSLTSLSGKMSASKPETAIVLTDSPEDVEKVKWFALTG 283
 Qy 333 GRTTIEERHOFGGCNDVUSPMWLTFFEDDKLQEIRKDY--TSGAMLGTGALKALIE 389
 Db 284 GRBTLLKEQREKGEBPEKCVVKMLEIFFEEDDK--KLKERYYACKNGEELTCGECKRYLISKIQEFLKERQRKK-AEKLVEFKYTG 341
 Qy 390 VQPLTIAEORRKEVTDIEVKEFMPRKL 411
 Db 342 KLOEFLKEHQKRKKAKOIEK 363

	Query Match	23.8%	Score 534.5;	DB 2;	Length 380;	
	Best Local Similarity	35.4%;	Pred. No. 1.2e-35;			
	Matches	141;	Conservative	76;	Mismatches	140;
					Indels	41;
					Gaps	17;
Y	33	AEDFPVDPWTWOTSSAKGIDYDKLIVRFGSSKIDKEKLINRERATGQRPHFLRRGIPPS	92			
b	3	ADGNIDVTPTVAVESDD--LDYEVKLARFGADELTDDQDARAP--DHPVLNRGIFYA	53			
b	93	HRDMMQVILDAVENKPKFLYTGGRGSSEAMEVGHFLIPITKWLQDVNPVNPLVQMTDDE	152			
b	54	GRDVDFLTTAGEOS---ITVGVGSG--PMLGHAMVYFARRLODEFGARVYVPLSDE	108			
b	153	KYLWKLDTLUDQAYGAVE-NAKDITACGFQNKTTF--SDLDNM-GMASGFYKNNVKI	207			
b	109	KYWFKDQTPAET-GDYLRLNDLIAVGFDPELTRIVDTRADLYPLATAFAGDV--	164			
b	208	QKHYVTFNQVKGIGFTSDCIGKTSFPATQAPSFSNSFPOIFRTRDQCLICPAIDQ	267			
b	165	-RHATIQNVG----EPDNVQAFYPAVQAHLL--LPQLVHG--EHEWLVPIALWDQ	213			
b	268	PYFRMTRDVAAPRIGP--KPALHSTFPALQAGTQKMSADPNSSIPLTDQAKIKTKV	325			
b	214	PHVRVSRVDAKARYPVGKCGALLMOPFLPLAG-PGKMS--AGVSIRLSDPDTWKRV	271			
b	326	NKHAFSGGRGTTIEEROFGGNCDVPSFWMLTFFEDDD-KLEQIRKDYSGAMTGEELK	384			
b	272	RTHAYTGGRASVEEHRAKGGVPAEDVPPFOQISAFFPDDAELARIEREYRAGDLISGELK	331			
b	385	KALEVLQPLAHSQARRKEVTEVKEFMPRKLSFD	422			
b	332	DLAADRITTEFLAAHORRRAALGD--VTEALDAFRLLTD	367			
	RESULT	11				
Y	64476	RYPTOPHAN-tRNA ligase (EC 6.1.1.2) - Methanococcus jannaschii				
	Alternate names:	tryptophanyl-tRNA synthetase				
	Species:	Methanococcus jannaschii				
	Date:	13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jun-2002				
	Accession:	F64476				
	Author(s):	Kane, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Wosse, C.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii; Reference number: A64300; NUID:96337999; PMID:8688087				
	Accession:	F64476				
	Status:	preliminary; nucleic acid sequence not shown; translation not shown				
	Molecule type:	DNA				
	Residues:	1-370 <BUL>				
	Genetics:					
	Cross-references:	GB:AB000812; GB:AB000666; NID:92621298; PIDN:AAB84757.1; PID:9262131				
	Experimental source:	strain Delta H				
	Gene:	MRH251				
	Start codon:	TTC				
	Superfamily:	mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology				
	Keywords:	aminoacyl-tRNA synthetase; ligase; protein biosynthesis				
	Query Match	17.7%	Score 397.5;	DB 2;	Length 364;	
	Best Local Similarity	27.9%;	Pred. No. 1.6e-24;			
	Matches	107;	Conservative	76;	Mismatches	153;
					Indels	47;
					Gaps	14;
QY	38	QVLPWTWOTSSAKGIDYDKLIVRFGSSKIDKEKLINRERATGQRPHFLRRGIFPSHRDMN	97			
Db	2	IDPW---GSAK-LYQDLDIENFGVPRP SEVLDDEV---PERSWLMRGGIIFGRHDYE	50			
QY	98	QVLDAYENKPKFLYTGGRGSSEAMEVGHFLIPETKWLQDVNPVLVQMTDDEKYLWK	157			
Db	51	RIISAMKKGEDPAVYVGMMSGR MAIGHMIVDOLRW YDRMMGAEFIFIADMEYASR	108			
QY	158	DILTDOAYDAVEN AKDIACGPINK-----TIFISDLYMGMSGFFYKNNVK	206			
Db	109	GYFDFEDSRRAIEVYTAGY ALGGLOLEKONIHYVQLOSENIVDLYAV-----	156			
QY	207	IOKHVTFNQVKGIGFTSDCIGKTSFPQAQABSFNSFPOIFRTRDQCLICAIQ	266			
Db	157	LAGKCNPNELRAIYGTGSTSMAMHAPIQVSDIHLQDLEGSPR--PVIVVGPQD	213			
QY	267	DYFRMTRDVAAPR---CYPKAHLHSTFPALQAGTQNSASUPNSIPLTDQAKIK	322			
Db	214	DPHTRLTDRAAFDRYGTLPSTSYYTRHMGFLGG--KNSSNPKSAFLPSDEEAE	271			
QY	323	TKVNGKAFFSGGRDTEHROFGGNCDVDSFMYLTFFLE-DDDKLQIRKDYTSQMLTG	381			
Db	272	AKI-RNAKIGGREGTKEQRLGGVPEECIYETIYHMGSGSDSRLLEEIVESCRNTLMCG	330			
QY	382	EIKKALIEVQOPLAHEQARKE	404			

Db 331 ECKNNTAEPFIRKPFEEELSVKREK 353
RESULT 13
 C;Species: Encephalitozoon cuniculi (fragment)
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 03-Jun-2002
 C;Accession: T43806
 R;Peyretailade, E.; Brionsoille, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.
 Mol; Biol. Evol. 15, 683-689, 1998
 A;Title: Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene
 A;Reference number: 222693; MUID: 98277683; PMID: 9615449
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-134 <PBY>
 A;Cross-references: EMBL:AJ012470; PIDN:CAA10034.1
 C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
 C;Keywords: ligase
 Query Match 17.2%; Score 386; DB 2; length 134;
 Best Local Similarity 51.5%; Pred. No. 3; 2e-24; Mismatches 35; Indels 4; Gaps 1;
 Matches 68; Conservative 25; MisMatches 35; Indels 4; Gaps 1;
 Qy 35 EDIFDVDTWQVQSSAK---GIDYDKLIVRFGSSSKIDKLINRERATGQRPHFLRRGIF 90
 Db 3 EQRITPDVEVSVTDEVPAVIDYDKLQNQFGCEKFNQALADRLEKLUSKGPKAHYERRGIV 62
 Qy 91 FSHRDMMQVLDAYENKKPFYLTYGRGSSEAMHVGHLIPFFTKWQDVFVNPLVIQMD 150
 Db 63 FAHRDENLILDEBTAANRPPVLYTGREGSSKHMIGHNTPFLICKWQDAKFRKLVQITD 122
 Qy 151 DEKYLNKDLTD 162
 Db 123 DÉKFLWKSMRLIE 134

RESULT 14
 E69461 TRYPTOPHANYL-tRNA synthetase (trps) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Accession: E69461
 R;Klemk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Quackenbush, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
 A;Authors: Utterback, T.R.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon, Archaeoglobus fulgidus A;Accession: E69461
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-374 <KAW>
 A;Cross-references: DDBJ:AP000064; MIG:95105945; PIDN:BAA81476.1; PID:95106165
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE2461
 C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase :repeat homology
 Query Match 15.7%; Score 353; DB 2; Length 374;
 Best Local Similarity 30.4%; Pred. No. 6.7e-21; Mismatches 165; Indels 38; Gaps 17;
 Matches 119; Conservative 70; MisMatches 165; Indels 38; Gaps 17;
 Qy 38 VDPWTWQTSKAKGIDYDKLIVRFGSSSKIDKLINRERATGQRPHFLRRGIFSHRDNN 97
 Db 8 LDPW---GAVEIKOYDRLLRTFGRPSEVL--PLRKAGMEPSLMLRGIIFGRDFD 61
 Qy 98 QVLPWTWQTSKAKGIDYDKLIVRFGSSSKIDKLINRERATGQRPHFLRRGIFSHRDNN 156
 Db 62 KILEAKARGERGVAVLTGFMPSGK_FHFGKLTVDOLIVLQNGFKV--FVAIADEAFAV 118
 A;Cross-references: GB:AE000986; GB:AE000782; MIG:92689309; PIDN:ABA99554.1; PID:9264885
 C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
 Query Match 16.5%; Score 370.5; DB 2; Length 420;
 Best Local Similarity 27.3%; Pred. No. 3e-22; Mismatches 118; Indels 89; Gaps 12;
 Matches 166; Conservative 60; MisMatches 166; Indels 89; Gaps 12;
 Qy 38 VPWPWTWQTSKAKGIDYDKLIVRFGSSSKIDKLINRERATGQRPHFLRRGIFSHRDNN 97
 Db 3 VTPWEVEGV---IDVSKLIEFGFMQP--SEVLPED---NPHLMRGAIIFGHDY 52
 Qy 215 QVKGIFG-FFTSDCIGKISPAQAPSFSNSPQIFRRTDIQCLPACIADOPYFRMT 273
 Db 175 EMEAIGETPAKOMSLT---QADILHVQDLYBGGF--HVVPVPGADOPHLRI 227
 Qy 274 RDVAR---IGYKPALLISTFPALOAQTKNSASDNNSIETDTQKIKVUNKA 329
 Db 228 RDLADMAGVWELERPASTVHKLQGLD3---RKMSSRPUFDSTFLDPPEVARNLFR_A 284
 Qy 330 FSGGRDTIESHQFGNCDY-DVSMVLUFPLEDDKLUQIRKOTS---GAMITGELKK 385
 Db 285 LTGGRATAEORRUGVPGVPCSVYNDLTHLMPDGEVKII--YTSCUQKILGECCT 341
 Qy 158 DILTDQAYGDAVENAKOIIACCFDINKTFIFSDLDYMGMSGFYKNUV-KIQKHTFNFQV 216

Fri Jul 11 11:50:10 2003

us-09-813-718-10_copy_48_471.rpr

Page 8

QY 386 ALIBVLOPLAEMOARRKEVTDEIVKEFMTPR 417
| : | : | : | : |
Db 342 IAWEKLERFLAEMHOSRLSKAKTIAWKLUVEPPR 373

Search completed: July 10, 2003, 12:32:17
Job time : 18.4461 secs

us-09-813-718-10_copy_48_471.rsp

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OM protein - protein search, using sw model

Run on: July 10, 2003, 12:26:29 ; Search time 9.25091 Seconds
(without alignments)

Maximum DB seq length: 1900.998 Million cell updates/sec

Title: US-09-813-718-10_COPY_48_471

Perfect score: 2246

Sequence: 1 MSYKAAGEDYKADCPPGNP.....VTDIEIVKPFMTPRKLSPDFQ 424

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2231	99.3	471	1 SYW_HUMAN	P23381 homo sapien
2	2134.5	95.5	475	1 SYW_BOVIN	P17248 bos taurinus
3	2056	91.5	475	1 SYW_RABIT	P23612 oryctolagus
4	2032	90.5	481	1 SYW_MOUSE	P32921 mus musculus
5	1210	53.9	395	1 SYW_SCHEO	Q9692 schizosaccharomyces pombe
6	1163	51.8	432	1 SYW_C_YEAST	Q12109 saccharomyces cerevisiae
7	910.5	40.5	381	1 SYW_SULFO	Q976ml sulfolobus
8	905	40.3	380	1 SYW_SULFO	Q97zx0 sulfolobus
9	803	35.8	385	1 SYW_PYRAB	Q9uy11 pyrococcus
10	796	35.4	386	1 SYW_PYRHO	Q95b84 pyrococcus
11	735	32.7	375	1 SYW_PYRAB	Q8ztu5 pyrococcus
12	534.5	23.8	380	1 SYW_HALM1	Q9hn66 halobacterium
13	409.5	18.2	370	1 SYW_MEUTA	Q98810 methanococcus
14	397.5	17.7	364	1 SYW_METH	Q62352 methanobacter
15	386	17.2	134	1 SYW_ENCCU	Q96771 encephalitozoon cuniculi
16	370.5	16.5	420	1 SYW_ARCPE	Q28579 archaeoglobus fumiferans
17	353	15.7	374	1 SYW_AERPE	Q9Y924 aeropyrum
18	299.5	13.3	426	1 SYW_THERV	Q978y0 thermoplasm
19	268.5	12.0	426	1 SYW_THRA	Q9hiw5 thermoplasm
20	192	8.5	323	1 SYW_ARCFU	Q29482 archaeoglobus fumiferans
21	185.5	8.3	341	1 SYW_STPRN	Q97n42 streptococcus
22	182.5	8.1	340	1 SYW_STPRY	Q99xn4 streptococcus
23	175.5	7.8	341	1 SYW_CLOLO	Q46127 clostridium
24	174.5	7.8	341	1 SYW_LACLA	Q9cjdl lactococcus
25	172	7.7	394	1 SYW_YEAST	P36421 saccharomyces cerevisiae
26	170.5	7.6	366	1 SYW_SULFO	P95982 sulfolobus
27	169	7.5	395	1 SYW_AQUAE	Q67115 aquifex aegyptii
28	166.5	7.4	346	1 SYW_CHLTR	Q84589 chlamydial
29	163.5	7.3	353	1 SYW_BORBU	Q51038 borrelia burgdorferi
30	159.5	7.1	337	1 SYW_TREPA	Q83640 treponema pallidum
31	158	7.0	346	1 SYW_CHLMD	Q9pjfs chlamydia pneumoniae
32	152	6.8	344	1 SYW_CHLPM	Q9za74 chlamydia pneumoniae
33	6.5		1 SYW_HELPY	P56396 helicobacter	

ALIGNMENTS

34	13.8	6.1	319	1 SYW_METTH	O27795 methanobacter
35	136.5	6.1	528	1 SYW_BOVIN	Q29465 bovis taurus
			328	1 SYW_THEME	Q9wv2 thermogaea
36	135.5	6.1	328	1 SYW_BACST	P0053 bacillus st
37	133	5.9	343	1 SYW_MTCLE	Q49301 mycobacterium
38	132.5	5.9	528	1 SYW_HUMAN	P54377 homo sapiens
39	132.5	5.9	326	1 SYW_HELIP	Q9zx4 helicobacte
40	130	5.8	401	1 SYYC_SCHPO	Q1455 schizosaccharomyces pombe
41	129	5.7	379	1 SYWM_YEAST	P4040 haemophilus
42	128.5	5.7	334	1 SYW_HAEIN	P4335 mycoplasma
43	128	5.7	350	1 SYW_MCGGE	P46579 caenorhabditis elegans
44	124.5	5.5	347	1 SYW_MCGEE	
45	122	5.4			

RA Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kisseelev I.L.;
 RT "The human gene encoding tryptophanyl-tRNA synthetase: interferon-
 response elements and exon/intron organization.";
 RL Gene 128:237-245(1993).
 RN [7]
 RP SEQUENCE OF 265-276; 278-295; 299-317 AND 350-365.
 RC TISSUE=Keratinocytes; MEDLINE=9316043; PubMed=1208667;
 RX RAESMUNSEN H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969 (1992).
 RN [8]
 RP FUNCTION
 RX MEDLINE=92225128; PubMed=1373391;
 RA Bange F.-C., Flohr T., Buwitt U., Boettger E.C.;
 RT "An interferon-induced protein with release factor activity is a
 tryptophanyl-tRNA synthetase.";
 RL FEBS Lett. 300:167-166(1992).
 CC -- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- INDUCTION: BY INTERFERON GAMMA.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 or send an email to license@ebi.ac.uk).
 CC

DR EMBL; M77804; AA67324; 1; -
 DR EMBL; X59892; CAA42545; 1; -
 DR EMBL; M61715; ARAB1298; 1; -
 DR EMBL; X62570; CA44450; 1; -
 DR EMBL; S82905; ARB9393; 1; -
 DR EMBL; X67920; CAB94198; 1; -
 DR EMBL; X67921; CAB94198; 1; JOINED.
 DR EMBL; X67922; CAB94198; 1; JOINED.
 DR EMBL; X67923; CAB94199; 1; -
 DR EMBL; X67924; CAB94199; 1; JOINED.
 DR EMBL; X67925; CAB94199; 1; JOINED.
 DR EMBL; X67926; CAB94199; 1; JOINED.
 DR EMBL; X67927; CAB94199; 1; JOINED.
 DR EMBL; X67928; CAB94199; 1; JOINED.
 DR PIR; A41706; A41706.
 DR PIR; A41633; A41633.
 DR PIR; JH0533; JH0533.
 DR PIR; S1926; S19246.
 DR Aarhus/Ghent-2DPAGE; 3524; IEF.
 DR PRC1-2DPAGE; P23381; -
 DR Gene; HGNC; 12729; WARZ.
 DR MIM; 191050; -.
 DR InterPro; IPR002306; TIP tRNA-synt_1b.
 DR InterPro; IPR000738; WHEP-TRS.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR005459; WHEP-TRS; 1.
 DR Pfam; PF00579; tRNA-synt_1b; 1.
 DR PRINTS; PR01039; TRNAsYNTHRP.
 DR TIGRFAMS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP TRS; 1.
 KW Aminocyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT DOMAIN 19 64 "HIGH" REGION.
 FT SITE 164 173 "KNSKS" REGION.
 FT CONFLICT 213 214 SY -> GD (IN REF. 3).
 FT CONFLICT 424 424 A -> R (IN REF. 4).

SQ SEQUENCE 471 AA; 53165 MW; E9634449053A000 CRC64;
 SQ Query Match 99.3%; Score 2231; DB 1; Length 471;
 SQ Best Local Similarity 99.5%; Pred. No. 6.9e-177; Indels 0; Gaps 0;
 SQ Matches 422; Conservative 0; Mismatches 2; Gaps 0;
 QY 1 MSYKAAGEDYKADCPGCGPAFTSNHGFDATATEABEDVDPWVQFSSAKGIDYDKLJWRF 60
 DB 48 MSTKAAGEDYKADCPGCGPAFTSNHGFDATATEABEDVDPWVQFSSAKGIDYDKLJWRF 107
 QY 61 GSSKIDKLINRLERATGQRPHPLRKIGFFSHRDMMQVLDAYENKPFYLTGRGPSE 120
 DB 108 GSSKIDKLINRLERATGQRPHPLRKIGFFSHRDMMQVLDAYENKPFYLTGRGPSE 167
 QY 121 AMEVGHLLPPIFPKWMLQDVENVPLVQTMQDDEYLKDLTIDQAYDAVENAKDIAFG 180
 DB 168 AMEVGHLLPPIFPKWMLQDVENVPLVQTMQDDEYLKDLTIDQAYDAVENAKDIAFG 227
 QY 181 DINKTFPSFLDMGMGSSGFYKVNWKIQKHTVNQVKHNGFQKIGFTSDCIGKISPPAQAP 240
 DB 228 DINKTFPSFLDMGMGSSGFYKVNWKIQKHTVNQVKHNGFQKIGFTSDCIGKISPPAQAP 287
 QY 241 SFNSNPQIPIRDTQCLIPCAIDODPYPRMTDVARPGYPKALHSFPALQGAQ 300
 DB 288 SFNSNPQIPIRDTQCLIPCAIDODPYPRMTDVARPGYPKALHSFPALQGAQ 347
 QY 301 TKSASIPNNSFLTDPAQIKVNUHAFSGCRDTEHROFGGMCDVDYFSMVLTFEL 360
 DB 348 TKSASIPNNSFLTDPAQIKVNUHAFSGCRDTEHROFGGMCDVDYFSMVLTFEL 407
 QY 361 EDDKQFOIRKQYTSQAMLTGELKKALIEVLOPLAEHQARRKEVTDIEVGFPMTRKLS 420
 DB 408 EDDKQFOIRKQYTSQAMLTGELKKALIEVLOPLAEHQARRKEVTDIEVGFPMTRKLS 467
 QY 421 FDFQ 424
 DO 468 FDFQ 471

RESULT 2
 SW_BOVIN
 ID SW_BOVIN STANDARD PRT; 475 AA.
 AC P17248;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (TRPS)
 GN WARS.
 OS Bos taurus (Bovine).
 OC Bovidae; Metacida; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI TaxID:9913;

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Retina;
 RX MEDLINE=91329348; PubMed=190747;
 RA Garret M., Rajot B., Trezequet V., Labouesse J., Merle M.,
 RA Gander J.-C., Benedicto J.-P., Salafaranne M.-L., Alterio J.,
 RA Gueguen M., Sarger C., Labouesse B., Bonnet J.;
 RT "A mammalian tryptophanyl-tRNA synthetase shows little homology to
 prokaryotic synthetases but near identity with mammalian peptide
 chain release factor.";
 RT Biochemistry 30:7805-7817(1991).
 RN [2] SEQUENCE OF 17-475 FROM N.A.
 RC TISSUE=Pancreas;
 RA Garret M., Trezequet V., Pajot B., Gander J.-C., Merle M.,
 RA Gueguen M., Benedicto J.-P., Sarger C., Alterio J., La Bouesse B.,
 RA Labouesse J., Bonnet J.;
 RA Submitted (MAR 1990) to the EMBL/GenBank/DDBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +

CC diphospho + L-tryptophanyl-tRNA(Trp).

CC -!- SUBUNIT: HOMODIMER.

CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

CC -!- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.

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CC

CC DR ITPR002306; TRP tRNA-synt_1b.

CC DR InterPro; IPR000738; WHEP-TRS.

CC DR InterPro; IPR002335; tRNA-synt_1b.

CC DR InterPro; IPR001412; tRNA-synt_1.

CC DR Pfam; PF00458; WHEP-TRS; 1.

CC DR Pfam; PF00579; tRNA-synt_1b; 1.

CC DR PRINTS; PRO1039; TRNASYNTHTRP.

CC DR TIGR00233; tRPS; 1.

CC DR PROSITE; PS00118; AA_tRNA_LIGASE_I; 1.

CC DR PROSITE; PS00762; WHEP_TRS; 1.

CC KMSK Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.

CC DOMAIN 24 69 WHEP-TRS.

CC DOMAIN 1 17 DISPENSABLE_TO THE CATALYTIC ACTIVITY.

CC SITE 169 178 "HIGH" REGION.

CC SITE 353 357 "KMSKS" REGION.

CC CONFLICT 17 17 L -> M (IN REF. 2).

CC SEQUENCE 475 AA; 53729 MW; F7E531750137E832 CRC64;

Query Match Best Local Similarity 95.0%; Score 2134.5; DB 1; Length 475; Matches 402; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy 2 SYKAAGEDYKADCPGNPAPTSNKGDATEAEEDFVDMWVTQSSAKGIDYDKLIVRFG 61
Db 54 SYKAAGEDYKADCPGNPAPTSNKGDATEAEEDFVDMWVTQSSAKGIDYDKLIVRFG 113

Qy 62 SSKIDKEKLNRITERATGQRPHFLRGIFFSRDMNOVDALEYENKEPFYLYTGRGÉSEA 121
Db 114 SSKIDKELNRLRITERATGQRPHFLRGIFFSRDMHQIOLDAYENKEPFYLYTGRGÉSEA 173

Qy 122 MFTVGHLIPFIFTKWLODVFNTEVFLVONTDDCYLWKDQLTLQAGPAVENAKRDIACGFD 181
Db 174 MFTVGHLIPFIFTKWLODVFNTEVFLVONTDDCYLWKDQLTLQAGPAVENAKRDIACGFD 232

Qy 182 INKTFPSDLXGMMSGFYKVNWKQOKHVTMENQVKIGFTIDSCIGKSPAQAPS 241
Db 233 INKTFPSDLXGMMSGFYKVNWKQOKHVTMENQVKIGFTIDSCIGKSPAQAPS 292

Qy 242 FSNSPPOIFRDTIDCILQCAIDQDPYFRMRDVAPRIGYKPALLHSPTFPALOGAQ 301
Db 293 FSNSPPOIFRDTIDCILQCAIDQDPYFRMRDVAPRIGYKPALLHSPTFPALOGAQ 352

Qy 302 KNSASDRNSSLITLDTAKQIKTKVNKAFASSGRDTIBEHRRGGNGCDVDVSFMYLTFLE 361
Db 353 KNSASDPNSSTFLTDATAKQIKTKVNKAFASSGRDTIBEHRRGGNGCDVDVSFMYLTFLE 412

Qy 362 DDDKLGDRKTKTGTSGAMLTGEKKALJEVQLPLAHOARKEKVTDIYERFMTTRKLSF 421
Db 413 DDDKLGDRKTKTGTSGAMLTGEKKALJEVQLPLAHOARKEKVTDIYERFMTTRKLSF 472

Qy 422 DFO 424
Db 473 DFO 475

SYW_RABIT

ID SYW_RABIT STANDARD

PRT; 475 AA.

AC P23612; 028607;

DT 01-NOV-1991 (Rel. 20, Created)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DB Tryptophanyl-tRNA Synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TRPRS).

GN WARS

OS Oryctolagus cuniculus (Rabbit).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TAXID=9986;

[1] -

SEQUENCE FROM N.A.

RX MEDLINE=90239043; PubMed=2185472;

RX Lee C.C., Craigie W.J., Munzly D.M., Harlow B., Caskey C.T.;

RX "Cloning and expression of a mammalian peptide chain release factor with sequence similarity to tryptophanyl-tRNA synthetases.";

RX Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).

RX [2]

RX REVISIONS TO 169-174 AND 227-228, AND FUNCTION.

RX MEDLINE=94009608; PubMed=8404867;

RX Prolova L.Y., Dalphin M.E., Justesen J., Powell R.J., Drugeon G.,

RX McCaughey K.K., Kisselov L.L., Tate W.P., Haenni A.-L.,

RX "Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are distinct proteins.";

RX EMBO J. 12:4013-4019(1993).

CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +

CC diphosphate + L-tryptophanyl-tRNA(Trp).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

CC -!- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.

CC -!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE AN EUKARYOTIC RELEASE FACTOR (ERF).

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CC

CC DR ITPR002306; TRP tRNA-synt_1b.

CC DR InterPro; IPR000738; WHEP-TRS.

CC DR InterPro; IPR002305; tRNA-synt_1b.

CC DR InterPro; IPR001412; tRNA-synt_1.

CC DR Pfam; PF00458; WHEP-TRS; 1.

CC DR Pfam; PF00579; tRNA-synt_1b; 1.

CC DR PRINTS; PRO1039; TRNASYNTHTRP.

CC DR TIGR00233; tRPS; 1.

CC DR PROSITE; PS00118; AA_tRNA_LIGASE_I; 1.

CC DR PROSITE; PS00762; WHEP_TRS; 1.

CC KMSK Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.

CC DOMAIN 23 68 WHEP-TRS.

CC SITE 168 177 "HIGH" REGION.

CC SITE 353 357 "KMSKS" REGION.

CC Query Match Best Local Similarity 91.5%; Score 2056; DB 1; Length 475; Matches 383; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

CC

CC DR ITPR002306; TRP tRNA-synt_1b.

CC DR InterPro; IPR000738; WHEP-TRS.

CC DR InterPro; IPR002305; tRNA-synt_1b.

CC DR InterPro; IPR001412; tRNA-synt_1.

CC DR Pfam; PF00458; WHEP-TRS; 1.

CC DR Pfam; PF00579; tRNA-synt_1b; 1.

CC DR PRINTS; PRO1039; TRNASYNTHTRP.

CC DR TIGR00233; tRPS; 1.

CC DR PROSITE; PS00118; AA_tRNA_LIGASE_I; 1.

CC DR PROSITE; PS00762; WHEP_TRS; 1.

RESULT 3

Db 113 SKIDKELVNRIERATGORPHFLRGLFFSHRDNNQVLDAYENKKPFYLYTRGRPSSEA 172
 QY 122 MHVGLHPLPITFKWILQDVNVPVLIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACFD 181
 CC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 173 MHYGHLLPITFKWILQDVNVPVLIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACFD 232
 QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 233 VNKTFIFSDLDYGMSPGFKVNVKIQKEVTFNQVKGIGFTSDCIGKISFFAIQAPS 292
 QY 182 INKTFIFSDLDYGMSPGFKVNVKIQKEVTFNQVKGIGFTSDCIGKISFFAIQAPS 241
 DR :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 DR PRINTS: PRO1039; TRNA-SYNT-TRP.
 DR TIGRFAMS; TIGR00233; TIGR00233; TIGR00233; TIGR00233;
 DR PROSITE: PS00178; AA: TRNA_LIGASE_I; 1.
 DR PROSITE: PS00762; WHEP_TRS; 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Alternative splicing.
 DR DOMAIN 23 68 WHEP-TRS.
 FT SITE 160 177 "HIGH" REGION.
 FT SITE 353 357 "RNSKS" REGION.
 FT VARSPLIC 476 481 MISSING (IN ISFORM 2).
 SQ 353 KMSASDPNNSIPLTDQKIKTKONKAESGRDTIEBHRQFGNCDDVDSFMVLTPE 412
 QY 362 DDDKLEQIRKDYYTSGAMLTGELKCALIEVLQPLIAEHQARKEVTDIEKEFMTPRKLS 421
 Db 413 DDKLEQIRKDYYTSGAMLTGELKCALIEVLQPLIAEHQARKEVTDIEKEFMTPRQLCF 472
 QY 422 DFQ 424
 DR 473 HYQ 475

RESULT 4

SYN_MOUSE STANDARD PRT: 481 AA.

ID_P22921; ID 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TRYPTOPHANYL-tRNA SYNTHETASE (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TrPs).

GN WARS OR WRS.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=9508226; PubMed=7932716;
 RA Pajot, B.; Sarger, C.; Bonnet, J.; Garret, M.;
 RT "An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells.",
 RT J. Mol. Biol. 242:59-603 (1994).
 CC -I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I- SUBUNIT: HOMODIMER (By SIMILARITY).
 CC -I- ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -I- TISSUE SPECIFICITY: The short isoform is widely expressed, the
 CC long form is found only in embryonic stem cells.
 CC -I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
 CC

RESULT 5

SYN_SCPO STANDARD PRT: 395 AA.

ID_S2W_SCPO AC 009692; ID 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DB putative tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TrPs).

GN SPAC2P-13C.

OS Schizosaccharomyces pombe (Fission yeast).
 OC Schizosaccharomyces pombe; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TAXID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 CC MEDLINE=972; PubMed=11859360;
 RC STRAIN=972;
 RK Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 DR InterPro; IPR000738; WHEP-tRNA-synt_1b.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR01412; tRNA-synt_1.
 DR Pfam; PF00458; WHEP-TRS; 1.
 DR Pfam; PF00579; TRNA-synt_1b; 1.
 DR PRINTS: PRO1039; TRNA-SYNT-TRP.
 DR TIGRFAMS; TIGR00233; TIGR00233; TIGR00233; TIGR00233;
 DR PROSITE: PS00178; AA: TRNA_LIGASE_I; 1.
 DR PROSITE: PS00762; WHEP_TRS; 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Alternative splicing.
 DR DOMAIN 23 68 WHEP-TRS.
 FT SITE 160 177 "HIGH" REGION.
 FT SITE 353 357 "RNSKS" REGION.
 FT VARSPLIC 476 481 MISSING (IN ISFORM 2).
 SQ 52 MSYKAAMGCEBEYKAGCPGPNTAGRNCDSDATKASEDWDWPWTVRTSSAKGIDYDQLIVQP 111
 DR 61 GSSKIDKELVNRIERATGORPHFLRGLFFSHRDNNQVLDAYENKKPFYLYTRGRPSSE 120
 DR 112 GSSKIDKELVNRIERATGORPHFLRGLFFSHRDNNQVLDAYENKKPFYLYTRGRPSSE 171
 QY 121 AMEVGHLIPPIFKWILQDVNVPVLIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACGF 180
 DR 172 AMEVGHLIPPIFKWILQDVNVPVLIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACGF 231
 DR 181 DINKTFLPSDLDYGMSPGFKVNVKIQKEVTFNQVKGIGFTSDCIGKISFFAIQAPS 240
 DR 232 DINKTFLPSDLDYGMSPGFKVNVKIQKEVTFNQVKGIGFTSDCIGKISFFAIQAPS 291
 QY 241 SFSNSPQQIFRRTDQCLICAIODDPYFMRDVARIGYPKALLSTFPALOGAQ 300
 DR 292 SFSNSPQQIFRRTDQCLICAIODDPYFMRDVARIGYPKALLSTFPALOGAQ 351
 DR 301 TWSASDPNNSIPLTDQKIKTKONKAESGRDTIEBHRQFGNCDDVDSFMVLTPE 360
 DR 352 TWSASDPNNSIPLTDQKIKTKONKAESGRDTIEBHRQFGNCDDVDSFMVLTPE 411
 DR 361 EDDDKLQEIRKDYYTSGAMLTGELKCALIEVLQPLIAEHQARKEVTDIEKEFMTPRKLS 420
 DR 412 EDDDKLQEIRKDYYTSGAMLTGELKCALIEVLQPLIAEHQARKEVTDIEKEFMTPRQLS 471
 DR 421 FPPQ 424
 DR 472 FHFO 475

Qy

30 A-T-E-A-B-E-E-D-V-D-P-M-T-V----Q-T-S-A-K-G-I-D-Y-K-L-I-V-R-E-G-S-S-K-I-D-K-E-L-L-I-N-R-E-T-A-G-Q-R-P-H-F 84

DR

TIGR4MS; TIGR00233; trps; 1.

Db

P00178; AA

LIGASE I: FALSE NEG

KW

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW

Complete proteome.

FT

SITE

82

"HIGH" REGION.

FT

SITE

90

"KNSKS" REGION.

FT

SQ

381 AA; 44718 MW; 109F5A56AF7D7159 CRC64;

SQ

Query Match

40.5%

Score

91.05;

DB

1

Length

381;

Best Local Similarity

50.5%;

Pred.

No.

7.9e-68;

Matches

189;

Conservative

63;

Mismatches

99;

Indels

23;

Gaps

9;

Best Local Similarity

50.5%;

Pred.

No.

7.9e-68;

Matches

189;

Conservative

63;

Mismatches

99;

Indels

23;

Gaps

9;

Best Local Similarity

50.5%;

Pred.

No.

7.9e-68;

Matches

189;

Conservative

63;

Mismatches

99;

Indels

23;

Gaps

9;

RESULT

7

SYN_SUSTO

STANDARD;

PRT;

381 AA.

SYN_SUSTO

STANDARD;

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE006677; ARK40778.1; ALT_INI.
 DR InterPro; IPR002306; TRP_tRNA-synt_1b.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR PFam; PF00579; tRNA-synt_1b; 1.
 DR PRINTS; PRO1039; TRANASYNTHTRP.
 DR TIGRFPS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE_NEG.
 DR Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 81 "HIGH" REGION.
 FT SITE 253 "KMSKS" REGION.
 SQ SEQUENCE 380 AA; 44691 MW; CF8344CF63883680 CRC64;

Query Match 40.3%; Score 905; DB 1; Length 380;
 Best Local Similarity 48.7%; Pred. No. 2_2e-67; Indels 24; Gaps 10;
 Matches 190; Conservative 68; Mismatches 108; Rndels 24; Gaps 10;

QY 34 EDFPVFDWVTPVQSSAKG-IDVYKLIVPGSSKIDKEILNRERATQRPHPHFLRRGFFS 92
 DB 57 HRLDLVLYNDYRSKSKGFLYTRGRAPSIL-GMHTGHLPFLPTWKLQERKPNANLYIRITDE 115
 DB 3 DFRFTVTPWEV----KGKVYKLIVPGTQKITEELKQRKINLAGDL-HVMLRNVFFS 56

QY 93 HRDMNQVLDAYENKKPFYLITGRGPSSSEAMHVGHLPPFTKWLQDVFNVLVIQMDDE 152
 DB 116 KYNRNPNTFTDQTRSWAYNDIIDIANGFNPKTFPIQDTEYI--RNMYTITVKAKL 172

QY 153 KLYWK-DLTLDAYGDAVENAKDIIAGCDFDINKTFPSDLDMGMSSGFYKVNVKQKHV 211
 DB 173 TFSERVATFGFLDASSNIGLIFYPALQIAPT-----MFEKK---RCLIPAGIDODPYWR 222

QY 272 MRDVARIGVYKPKALLHSTFPALOGAQTKMASDNNSTFLDTAQOKIKVNGHAFS 311
 DB 223 LQDRTAEGSLGYYKAQOHSKELPLPPTGREGKNSSNPETAIVLVDPPKTVRKIMYAFS 282

QY 332 GRDTBEHRQFGNCDDVSTMLTLEDD-KUBQIRKQYTSGAMLTCBLLKALIEV 390
 DB 283 GQOPTIELHKGOGNPEIDVPOWLYFPEEDNRKEIEEEYRSGKMLTGELKQIILDK 342

QY 391 LQPLTAHQARKKEVTIDVKEFMRTPKL 420
 DB 343 LMKFLEER-RRKEEAKLVHVFKYDGKLA 371

RESULT 9
 SYW_PYRAB STANDARD PRT; 385 AA.

ID SYW_PYRAB STANDARD PRT; 385 AA.

AC Q9Y11; DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (trps).
 GN TRPS OR PAR11.
 OS Pyrococcus abyssi.
 OC Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus; NCBI_TAXID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RA Heilig R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution.";
 RU Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -I CATALYTIC ACTIVITY: ARP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBCELLULAR LOCATION: Cytoplasmic
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE006677; ARK40778.1; ALT_INI.
 DR InterPro; IPR002306; TRP_tRNA-synt_1b.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR PFam; PF00579; tRNA-synt_1b; 1.
 DR PRINTS; PRO1039; TRANASYNTHTRP.
 DR TIGRFPS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE_NEG.
 DR A248288; CAB50601.1; --
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR PFam; PF00579; tRNA-synt_1b; 1.
 DR PRINTS; PRO1039; TRANASYNTHTRP.
 DR TIGRFPS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 82 "HIGH" REGION.
 FT SITE 253 "KMSKS" REGION.
 SQ SEQUENCE 385 AA; 45100 MW; 4C29D01414976B12 CRC64;

Query Match 35.8%; Score 803; DB 1; Length 385;
 Best Local Similarity 45.3%; Pred. No. 6.2e-59; Indels 26; Gaps 9;
 Matches 173; Conservative 63; Mismatches 120; Rndels 26; Gaps 9;

QY 35 EDF-VDPWVTPVQSSAKGIDKYLIVPGSSKIDKEILNRERATQRPHPHFLRRGFFSH 93
 DB 3 EDFKVLPFWVEGV---VDVNLKIEHFGSPSPLTEBLEKTAKLTSLEPLFRRKFFFSH 58

QY 94 RDMMNQVLDAYENKKPFYLITGRGPSSSEAMHVGHLPPFTKWLQDVFNVLVIQMDDE 153
 DB 118 FLFKENLTFEDTKHAYENNDIANGFDDKTFIQNSER---TKVEMAIIPIAKIN 173
 DB 59 RDYKVQIQLDVEEGRGFLYTRGRGPQ-PMHIGHTIPPAFTKWLQERKFGVNLQIOTIDBK 117

QY 154 VLKWD-LTLDAYGDAVENAKDIIAGCDFDINKTFPSDLDMGMSSGFYKVNVKQKHV 212
 DB 174 FSAKAVVGFIFEQSKIGMIFPPAIQIAPT-----FEGR---RCLIPAGIDODPYWR 223

QY 273 TRDVARIGVYKPKALLHSTFPALOGAQTKMASDNNSTFLDTAQOKIKVNGHAFS 332
 DB 224 QRDFAESLGYYKTAATHSKFVPSLTSLSGKMSASKPETAIVLTDPSPEDVKKWKFALIG 283

QY 333 GRDTBEHRQFGNCDDVSTMLTLEDD-KUBQIRKQYTSGAMLTCBLLKALIEV 389
 DB 284 GRPTLQEKRKGEBEBCVWPKWLEFSDK--KLKERYAACQIEK 341

QY 390 VQPLTAHQARKKEVTIDVKEFMRTPKL 411
 DB 342 KIOEFLIKEHQGRKKAQKIEK 363

RESULT 10
 SYW_PYRHO STANDARD PRT; 386 AA.

ID SYW_PYRHO STANDARD PRT; 386 AA.

AC Q9Y54; DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (trps).
 GN TRPS OR PH1921.

OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcidae;
 OX NCBI_TaxID=53953;
 RN [1]
 SSQUENCE FROM N.A.
 RP STRAIN=OT3;
 RX PMID=98341137; PubMed=9679194;
 RA Kawarabayasi Y.; Sawada M.; Horikawa H.; Haikawa Y.; Hino Y.; Nagai Y.;
 RA Yamamoto S.; Sekine M.; Baba S.-I.; Kobugi H.; Hosoyama A.; Nagai Y.;
 RA Sakai M.; Ogura K.; Otsuka R.; Nakazawa H.; Takamiya M.; Ohfuki Y.;
 RA Funahashi T.; Tanaka T.; Kudo Y.; Yamazaki J.; Kubisida N.; Oguchi A.;
 RA Aoki K.-I.; Yoshizawa T.; Nakamura Y.; Robb P.T.; Horikoshi K.;
 RA Masuchi Y.; Shizuya H.; Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeabacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998);
 CC -I CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC
 DR EMBL; AP00007; BRA31046.1; ALT INIT.
 DR InterPro; IPR002206; Trp tRNA-Synt_1b.
 DR InterPro; IPR002305; tRNA-Synt_1b.
 DR PRINTS; PR00579; TRNA-SYNT1B_1.
 DR PROSITE; PS00139; TRNSYNTHPRP.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 82 90 "HIGH" REGION.
 FT SITE 253 257 "KMSKS" REGION.
 SQ SEQUENCE 386 AA; 45305 MW; 983C32F4028B2DD CRC64;

Query Match 35.4%; Score 796; DB 1; Length 386;
 Best Local Similarity 44.0%; Pred. No. 2.4e-58; Mismatches 125; Indels 26; Gaps 9;
 Matches 172; Conservative 68; Mismatches 125; Indels 26; Gaps 9;
 Oy 34 EEPKVDPWPMVQISSAKGIDYDVKLIVREGRSSKKIDELINRIRATGQRPHFRRGIFPSH 93
 .Db 3 EEPKVDPWPMVQISSAKGIDYDVKLIVREGRSSKKIDELINRIRATGQRPHFRRGIFPSH 58
 .Db 94 RDMDAQVLDAYENKKPPFLYTGRRGSSEAMVGHGLIPFFTKMIDQDVNVPLVLIQMTDEK 153
 .Db 59 RYDYLILKDYEBRGFLYTGPGSG-EWPHIGHIIPEFAKTMQLEKGVNVIQIQTDEK 117
 Qy 154 YLWGD-LTDQAYGDAVENAKDIAAGDINKPPIFSQDYMGMSSGFYKNVVKQHVT 212
 .Db 118 FLLKNULTFFDTGKEMAYDNILDIAVNGFDPKTPKTFIQNSEF---TKIYEMAIPIAKKIN 173
 Db 213 FQVQKGTRGFTSDCIGKISPAQIAQSFSNSFPQFDRDRDIQCLPCADQDPYFMR 272
 .Db 174 FSNKAVAFGFTEDOSKIGMIPFPQIAPTP-----PERK---RCUJPAATDODPYWRL 223
 Qy 34 RDPF-DPWPVTTQTSQSKIDDKLUTGPGSSKIDELINRIRATGQRPHFRRGIFPSH 92
 .Db 2 EEEFVTPWEVGR---VDYEKLKUHFGAKPLTKDDEVALLBKAGE-VHPLIRRGGFFIA 56
 Qy 93 HRDMQGQVLDAYENKKPPFLYTGRRGSSEAMVGHGLIPFFTKMIDQDVNVPLVLIQMTDE 152
 .Db 57 HRDFDFMVKHMGEGRIPWALYTGRRGS-PVHIGHMWPWILKWFSDRKGFLGLVQLTDDE 115
 Qy 153 K-YLWKDLTDQAYGDAVENAKDIAAGDINKPPIFSQDYMGMSSGFYKNVVKQHVT 211
 .Db 224 QDFAESLGYYKTAALISKFVSLTSLSGKMAWASKPETAIVLJDSPDVEKWKMFILTG 283
 Qy 333 GRTQIEERHQFGANCQDVSVFMLLTFEEDDKLQEQRKDY---TSGAMLTREBLKALIE 389
 .Db 284 GRFLIKEOREKGSESEPEKCVVKWLIEFFEDK---KUKERRYACKNGSLBITCGECCKYLIS 341
 Qy 390 VIOPLIAHOOARKKEVTDIIVEKFMPTRKL 420
 Db 342 KIQLFLKHORRKK-AEKLVKEPKYTGKA 371

RESULT 11
 SW_PIRAE
 ID SW_PIRAE
 STANDARD
 PRT; 375 AA.
 DT 08ZTUS;
 AC 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DR 15-JUN-2002 (Rel. 41, Last annotation update)
 DB Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (TRPLS)
 GN TRPLS OR PA33091
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 SSQUENCE FROM N.A.
 DR STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PMID=1172869;
 RA Fitz-Gibbon S.T.; Ladner H.; Kim U.-J.; Stetter K.O.; Simon M.I.;
 RA Miller J.H.;
 RR "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002)."
 DR -I CATALYTIC ACTIVITY: AMP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 modified and this statement is not removed. Usage by and for commercial/
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB00911; ALA4664.1; -.
 DR InterPro; IPR002306; Trp tRNA-Synt_1b.
 DR InterPro; IPR002305; tRNA-Synt_1b.
 DR InterPro; IPR001412; tRNA-Synt_1.
 DR TIGRFAMS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 81 89 "HIGH" REGION.
 FT SITE 258 262 "KMSKS" REGION.
 SQ SEQUENCE 375 AA; 43178 MW; 3DBBF85DA680F116 CRC64;

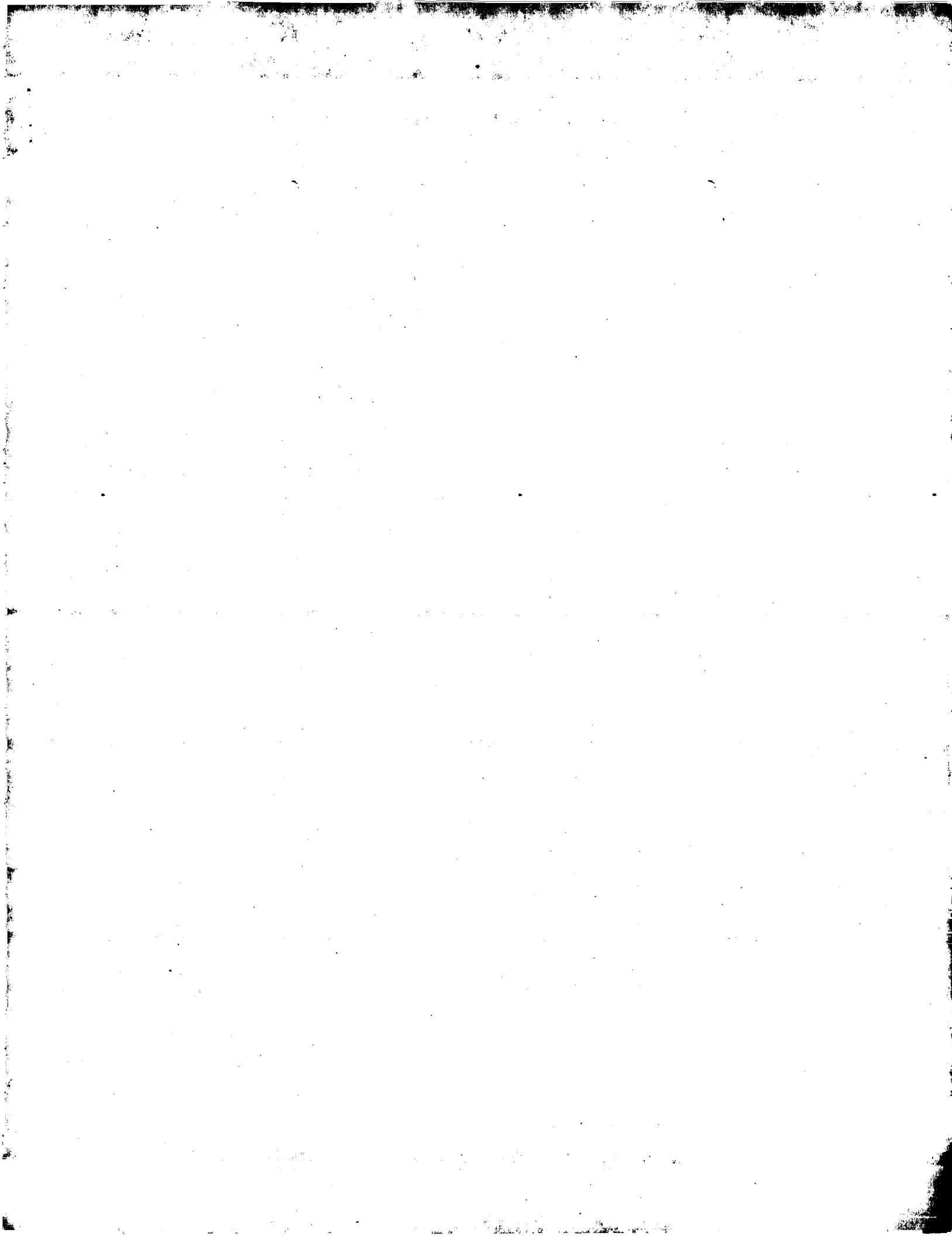
Query Match 32.7%; Score 735; DB 1; Length 375;
 Best Local Similarity 41.6%; Pred. No. 2.5e-53; Mismatches 130; Indels 18; Gaps 11;
 Matches 162; Conservative 79; Mismatches 130; Indels 18; Gaps 11;
 Oy 34 RDPF-DPWPVTTQTSQSKIDDKLUTGPGSSKIDELINRIRATGQRPHFRRGIFPSH 92
 .Db 2 EEEFVTPWEVGR---VDYEKLKUHFGAKPLTKDDEVALLBKAGE-VHPLIRRGGFFIA 56
 Qy 93 HRDMQGQVLDAYENKKPPFLYTGRRGSSEAMVGHGLIPFFTKMIDQDVNVPLVLIQMTDE 152
 .Db 57 HRDFDFMVKHMGEGRIPWALYTGRRGS-PVHIGHMWPWILKWFSDRKGFLGLVQLTDDE 115
 Qy 153 K-YLWKDLTDQAYGDAVENAKDIAAGDINKPPIFSQDYMGMSSGFYKNVVKQHVT 211
 .Db 116 KFYDDEMKLKEBATWAVENALDVIAGLFSPERLHLIITPKDI--KPLYPIAVRVAKU 172
 Qy 212 TENVQKGIGFGDFSDGKSFPAQQAAPSNSPFIQFRTDQCLLTCIAODPYR 271
 .Db 173 TWNTVKATGFTDSTWNLGFLYPPSLSLQIAVPLP---BLRERATPV--LPCAIQDOPYR 228
 Qy 272 MTRDVAIPRGPKPQALKHSTPFPAQOGAQTMASADPNSSFLTDQAKQTKVNUKAHS 331
 .Db 229 LARDIADLAGYKPKSTLYSKFIMALG-ESKMSASNPDSALVYTLDEDETVRKV-MNAPF 286

QY	332 GGRDITIEERHQFGCGNCDDVDFPMIITFLEDDKLEQIRKDYTGSGAMLTGELKKALIEVL 391	Db	54 GRDVDDFLTRGEQS ---IVTGVGPSG -PHILGHAMVFPRARRLODEFGARVVYPLSDBE 108
Db	287 GGRTPTAESORKYGGNPEVCPVFRHMLFDPDASVEKTRQDCKSGALLCGECKLHEKI 346	Qy	153 KYLWKLDTUDQAYDAVE-NAKDIACGFENDKNUPIF--SDLDOM-GMSSGFYKNVVKI 207
Qy	392 QPLIAEHQRKEVTDIYKEFMTPKLS 420	Db	109 KYWFKDQTPAET-GDYLRANLDRDILAVGFDPELTLVVDTRRADVLYPLATAFAGDV-- 164
Db	347 TKFLKEHRERKRGK-VDEYRUSVKLS 374	Qy	208 QKHTFPNQVKGIFGFTDSDCIGKISPPATQAPSPRSNSPQQIFRDRDYLQCLPCAIQDQ 267
Qy	09HN66; 15-JUN-2002 (Rel. 41, Created)	Db	165 -RHATLONVIG---EPDNVQAFYPAVQTHL--LPOLVH--EHETLVIAVDP 213
DT	15-JUN-2002 (Rel. 41, Last sequence update)	Qy	214 FHVRYSRDVAAKARYKPGKGAQMFIISLAG PGKMASS--AGVSIRLTDSPDVREK/ 271
DT	15-JUN-2002 (Rel. 41, Last annotation update)	Db	326 NKHAFSGGRDITIEERHQFGCGNCDDVDFPMIITFLEDDKLEQIRKDYTGSGAMLTGELK 384
DE	TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)	Db	272 RTHAYTGGRASVEBHRAKGGVPAEDVPOYLSAFAFPDDAELARIEREYRAGDLILLGELK 331
DE	(TRPS).	Qy	385 KALEVIQPLAHEQRKEVTDIYKEFMTPKLSFD 422
OS	TRPS OR TRP52 OR VNG233G.	Db	332 DLAADRTEFLAAHQRRRAALGD- VTEALDAFRILDD 367
OC	Halobacterium sp. (strain NRC-1).	OC	
OC	Archaea; Euryarchaeota; Halobacteria; Halobacteriales;	OC	
OC	Halobacteriaceae; Halobacterium.	OC	
NCBI_TaxID=64091;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2054483; PubMed=11016950;		
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,		
RA	Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrosga J.,		
RA	Swartzell S., Weir D., Hall J.J., Dahl T.A., Welti R., Goo Y.A.,		
RA	Leithauer B., Keiller K., Cruz R., Danson M.J., Hough D.W.,		
RA	Maddock D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,		
RA	Ibenbarger T.A., Peck F.R., Ponischroder M., Spudich J.L., Jung K.-H.,		
RA	Alam M., Fritts T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,		
RA	Ebbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,		
RA	"Genome sequence of Halobacterium species NRC-1." Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).		
RL	- - CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).		
CC	- - SUBCELLULAR LOCATION: Cytoplasmic.		
CC	- - SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.		
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RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	STRAIN=JM1-1 / DSM 2661 / ATCC 43067;		
RX	MEDLINE=96331999; PubMed=8688087;		
RA	Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,		
RA	Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,		
RA	Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,		
RA	Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,		
RA	Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,		
RA	Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hama M.C.,		
RA	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,		
RA	Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,		
RA	"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii." Science 273:1058-1073 (1996).		
RA	Science 273:1058-1073 (1996).		
RA	- - CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).		
CC	- - SUBCELLULAR LOCATION: Cytoplasmic.		
CC	- - SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.		
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FT	SITE 249 253 "KOSKS" REGION.		
FT	SEQUENCE 380 AA: 41936 MM: 07B2B955386404F CRC64;		
KW	Aminoacyl-tRNA synthetase; protein biosynthesis; ligase; ATP-binding; Complete proteome.		
FT	SITE 74 82 "HIGH" REGION.		
FT	SEQUENCE 380 AA: 41936 MM: 07B2B955386404F CRC64;		
QY	Query Match 23.8%; Score 53.4-5; DB 1; Length 380; Best Local Similarity 35.4%; Pred. No. 9.6e-37; Matches 141; Conservative 76; Mismatches 140; Indels 41; Gaps 17; SQ		
QY	33 AEEFDVDPVTQVSSAKGIDYKLUVFRGSSKIDKELINRIERATGQRPHFLRGIF 92	DR	153 KYLWKLDTUDQAYDAVE-NAKDIACGFENDKNUPIF--SDLDOM-GMSSGFYKNVVKI 207
Db	3 ADGNDVTPAVESDD--LDEYKLARFGADELTDQARFP----DHPLVNGLFYA 53	DR	109 KYWFKDQTPAET-GDYLRANLDRDILAVGFDPELTLVVDTRRADVLYPLATAFAGDV-- 164
QY	93 HRDMQVDAVENKKPFPLYTGREGSSEAMHGVLHIFIFTKWLQDVENVPLVQMTDE 152	DR	208 QKHTFPNQVKGIFGFTDSDCIGKISPPATQAPSPRSNSPQQIFRDRDYLQCLPCAIQDQ 267
DR	TIGR; MJ1415; -.	DR	214 FHVRYSRDVAAKARYKPGKGAQMFIISLAG PGKMASS--AGVSIRLTDSPDVREK/ 271
DR	InterPro; IPRO02305; Tp tRNA-synt_1b.	DR	326 NKHAFSGGRDITIEERHQFGCGNCDDVDFPMIITFLEDDKLEQIRKDYTGSGAMLTGELK 384
DR	InterPro; IPRO01412; tRNA-synt_I.	DR	272 RTHAYTGGRASVEBHRAKGGVPAEDVPOYLSAFAFPDDAELARIEREYRAGDLILLGELK 331
DR	Fam; PF00579; tRNA-synt_1b; 1.	DR	332 DLAADRTEFLAAHQRRRAALGD- VTEALDAFRILDD 367
DR	PRINTS; PRO1039; TRNASTNTHPR.	DR	
DR	TIGRFAMs; TIGR0033; tRNA_1.	DR	
DR	InterPro; IPRO02305; tRNA-synt_1b.	DR	
DR	Fam; PF00579; tRNA-synt_1b; 1.	DR	
DR	PRINTS; PRO1039; TRNASTNTHPR.	DR	
DR	PROSITE; PS001178; AA_tRNA_LIGASE_I; 1.	DR	
DR	Aminoacyl-tRNA synthetase; protein biosynthesis; ligase; ATP-binding; Complete proteome.	DR	
DR	SITE 249 253 "HIGH" REGION.	DR	
DR	SEQUENCE 380 AA: 41936 MM: 07B2B955386404F CRC64;	DR	
DR	Query Match 23.8%; Score 53.4-5; DB 1; Length 380; Best Local Similarity 35.4%; Pred. No. 9.6e-37; Matches 141; Conservative 76; Mismatches 140; Indels 41; Gaps 17; SQ	DR	
DR	33 AEEFDVDPVTQVSSAKGIDYKLUVFRGSSKIDKELINRIERATGQRPHFLRGIF 92	DR	
DR	3 ADGNDVTPAVESDD--LDEYKLARFGADELTDQARFP----DHPLVNGLFYA 53	DR	
DR	93 HRDMQVDAVENKKPFPLYTGREGSSEAMHGVLHIFIFTKWLQDVENVPLVQMTDE 152	DR	

RT "Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene of mitochondrial evolutionary origin.";
 RT Mol. Biol. Evol. 15:683-689 (1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophanyl-tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL; AJ012470; CAA10341; --.
 DR InterPro; IPR002305; tRNA-synt_I.
 DR IPR001412; tRNA-synt_I.
 DR Pfam; PF00579; tRNA_synt_1b; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 PT SITE 89 98 "HIGH" REGION.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 15744 MW; 60E2935B7E1E344F CRC64;

Query Match 17.2%; Score 386; DB 1; Length 134;
 Best Local Similarity 51.5%; Pred. No. 4 4e-25;
 Matches 68; Conservative 25; Mismatches 35; Indels 4; Gaps 1;
 Qy 35 EFPFDPTVQTSKAK---GIDYDKLIVTPRGSSKIDKEKLINIERATGQRPHFLRRGIF 90
 Db 3 ECRITPMDVEVNSTDEVPAVTDKIQFGERKENQALADRLKUSGKPAYFERRGIV 62
 Qy 91 FSHRNDMQLDVALYENKICPKFYLYTGGRGSSEAMAVGHLLPFTTKWLODVNVNPLVQMTD 150
 Db 63 FAHRDENVLLDIDIANNNRPFYLTGGRGSSEAMAVGHLLPFTTKWLODVNVNPLVQMTD 122
 Qy 151 DFKYLWKDLTLQ 162
 Db 123 DEKFPLWKSMLRQE 134

Search completed: July 10, 2003, 12:30:34
 Job time : 10.2509 secs



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OM protein - protein search, using sw model

Run on: July 10, 2003, 12:27:20 ; Search time 28.7806 Seconds
(without alignments)

3035.516 Million cell updates/sec

Title: US-09-813-718-10_COPY_48_471

Perfect score: 2246

Sequence: 1 MSYKAACEDDYKADCPPRN.....VTDIEIVKFEMTPRKLSPFDQ 424

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqB, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximun Match 100%

Listing first 45 summaries

Database : SPREMBL_21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_p rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriapl:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description	PRELIMINARY	PRT;	ALIGNMENTS
1	2051	91.3	475	11	Q9DC65	Q9DC65	475 AA.	
2	2047	91.1	481	11	Q9J58	Q9DC65; 01-JUN-2001 (T-BEMBLrel. 17, last sequence update)		
3	1629	72.5	329	11	Q9DR9	DT 01-JUN-2002 (T-BEMBLrel. 21, last annotation update)		
4	1537	68.4	305	11	Q9I84	DT Adult male lung cDNA, RIKEN clone:1200002C07, full insert sequence.		
5	1382	61.5	430	5	Q9I4Y1	DE		
6	1379.5	61.4	420	5	Q9I4Y0	RX MEDLINE=21085660; PubMed=11217851; STRAIN=C57BL/6J; TISSUE=LUNG; NCBI_TaxID=10050; RN [1]		
7	1378	61.4	430	5	Q9Hg2	RC SEQUENCE FROM N.A.		
8	1301	57.9	402	10	Q9SR15	RC		
9	1027	45.7	324	5	Q9U1R2	RC		
10	942	41.9	385	5	Q8qY5	RC		
11	826.5	36.8	385	17	Q8u453	RC		
12	800.5	36.6	490	5	Q9lf5	RC		
13	682	30.4	136	6	Q9295	RC		
14	453	20.2	374	17	Q8tyf7	RC		
15	388.5	17.3	136	6	Q9t88	RC		
16	329.5	14.7	437	17	Q8tua1	RC		

DR MGB; MGI:104630; Wars.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR InterPro; IPR002306; Trp_tRNA-synt_1b.
 DR InterPro; IPR000738; WHEP-TRS.
 DR Pfam; PF00519; tRNA-synt_1b; 1.
 DR Pfam; PF00438; WHEP-TRS; 1.
 DR PRINTS; PR01039; TRANSYNTHRP.
 DR TIGRFAMs; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP_TRS; 1.
 DR Sequence; 475 AA; 53541 MW; C3467FB85521DB4C CRC64;
 DR Sequence; 475 AA; 54325 MW; A754B1DDF58E2BF3 CRC64;

Query Match 91.3%; Score 2051; DB 11; Length 475;
 Best Local Similarity 90.3%; Pred. No. 4.9e-165;
 Matches 383; Conservative 21; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MSYKAAGEDDYKADCPGPNPAPTSNNGDATEAEEDFUDPMWQTSAAKGIDYDLYLURE 60
 Db 52 VSYKAAMGEDEYKAGCPPGNPPTAGRNCSDATKASEDFDVDPWTWRTSSAKGIDYDLYLUF 111
 Qy 61 GSSKIDKELINIRERATGQRPHFLRGIFPSHRDMNQVLDAYENKKPFYLTYGRGSE 120
 Db 112 GSSKIDKELINIRERATGQRPHFLRGIFPSHRDMNQVLDAYENKKPFYLTYGRGSE 171
 Qy 181 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 240
 Db 232 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 291
 Qy 241 SFNSNPSPQIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 300
 Db 292 SFNSNPSPKIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 351
 Qy 301 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 360
 Db 352 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 411
 Qy 361 EDDDKLEQIRKDTISGAMLTGELKKALIEVQLIAHQARRKEVTDIHKSPMTPRLS 420
 Db 412 EDDDKLEQIRKDTISGAMLTGELKKALIDVLOPLIAHQARRKAVTEETVKEMTPRLS 471
 Qy 421 FHFQ 424
 Db 472 FHFQ 475

RESULT 2

ID Q99J5B PRELIMINARY; PRT; 481 AA.

AC Q99J5B; Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)

DB Tryptophanyl-tRNA synthetase.

GN WARS.

OS Mus musculus (Mouse).

OC Bokaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID:10090;

RN [1] SEQUENCE FROM N.A.

RR STRAIN=CS57BL/6J; TISSUE=PANCREAS;

RR MEDLINE=2108560; PubMed=11217851;

RR Kawai J., Shingawa A., Shibasaki K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Boni H., Kasukawa T., Saito R., Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stauble F., Suzuki K., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., InterPro; IPR002305; tRNA-synt_1b.

DR InterPro; IPR001412; tRNA-synt_I.

DR InterPro; IPR00233; trps; 1.

DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.

DR PROSITE; PS00762; WHEP_TRS; 1.

DR Sequence; 481 AA; 54325 MW; A754B1DDF58E2BF3 CRC64;

Query Match 91.1%; Score 2047; DB 11; Length 481;
 Best Local Similarity 90.1%; Pred. No. 1.e-165;
 Matches 382; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MSYKAAGEDDYKADCPGPNPAPTSNNGDATEAEEDFUDPMWQTSAAKGIDYDLYLURE 60
 Db 52 VSYKAAMGEDEYKAGCPPGNPPTAGRNCSDATKASEDFDVDPWTWRTSSAKGIDYDLYLUF 111
 Qy 121 AMVGHILIPPIFTKWLQDVNVPLVLTQMTDDEKYLWQDLYTQDAVENAKDITACGF 180
 Db 172 AMVGHILIPPIFTKWLQDVNVPLVLTQMTDDEKYLWQDLYTQDAVENAKDITACGF 231
 Qy 181 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 240
 Db 232 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 291
 Qy 241 SFNSNPSPQIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 300
 Db 292 SFNSNPSPKIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 351
 Qy 301 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 360
 Db 352 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 411
 Qy 361 EDDDKLEQIRKDTISGAMLTGELKKALIEVQLIAHQARRKEVTDIHKSPMTPRLS 420
 Db 412 EDDDKLEQIRKDTISGAMLTGELKKALIDVLOPLIAHQARRKAVTEETVKEMTPRLS 471
 Qy 421 FHFQ 424
 Db 472 FHFQ 475

RESULT 3

ID Q9D8R9 PRELIMINARY; PRT; 329 AA.

AC Q9D8R9; Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DB Tryptophanyl-tRNA synthetase.

GN WARS.

OS Mus musculus (Mouse).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID:10090;

RN [1] SEQUENCE FROM N.A.

RR STRAIN=CS57BL/6J; TISSUE=PANCREAS;

RR MEDLINE=2108560; PubMed=11217851;

RR Kawai J., Shingawa A., Shibasaki K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Boni H., Kasukawa T., Saito R., Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stauble F., Suzuki K., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., InterPro; IPR002306; Trp_tRNA-synt_1b.

DR InterPro; IPR000738; WHEP-TRS.

DR Pfam; PF00579; tRNA-synt_1b; 1.

DR Pfam; PF00458; WHEP_TRS; 1.

DR PRINTS; PR01039; TRANSYNTTRP.

DR TIGRFAMs; TIGR00233; trps; 1.

DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.

DR PROSITE; PS00762; WHEP_TRS; 1.

DR Sequence; 481 AA; 54325 MW; A754B1DDF58E2BF3 CRC64;

Query Match 91.1%; Score 2047; DB 11; Length 481;
 Best Local Similarity 90.1%; Pred. No. 1.e-165;
 Matches 382; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MSYKAAGEDDYKADCPGPNPAPTSNNGDATEAEEDFUDPMWQTSAAKGIDYDLYLURE 60
 Db 52 VSYKAAMGEDEYKAGCPPGNPPTAGRNCSDATKASEDFDVDPWTWRTSSAKGIDYDLYLUF 111
 Qy 121 AMVGHILIPPIFTKWLQDVNVPLVLTQMTDDEKYLWQDLYTQDAVENAKDITACGF 180
 Db 172 AMVGHILIPPIFTKWLQDVNVPLVLTQMTDDEKYLWQDLYTQDAVENAKDITACGF 231
 Qy 181 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 240
 Db 232 DINKTFFISPLDGMGSSGFYKVNUKIQKHVNQVKGIFGFDSCIGKSPQAQ 291
 Qy 241 SFNSNPSPQIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 300
 Db 292 SFNSNPSPKIFRDTIQCILCAIDQDPYFRMTRDVAARRIGYKPAHLHSTPPALGAQ 351
 Qy 301 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 360
 Db 352 TKSASDPNSSIFLTDAKQIKTKVNUKAFGGDTEFEHRQFGNCVDVSPMLTFPL 411
 Qy 361 EDDDKLEQIRKDTISGAMLTGELKKALIEVQLIAHQARRKEVTDIHKSPMTPRLS 420
 Db 412 EDDDKLEQIRKDTISGAMLTGELKKALIDVLOPLIAHQARRKAVTEETVKEMTPRLS 471
 Qy 421 FHFQ 424
 Db 472 FHFQ 475

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Wynnshaw-Boriss A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsukii S.,
 RA Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 DR EMBL; AK00754; BAB5235.1; -.
 DR MGDB; MG1:04630; Wars.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002306; Trp_tRNA-synt_1b.
 DR Pfam; PF00579; tRNA-synt_1b; 1.
 DR PRINTS; PRO1039; TRNA-SYNTTRP.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 SQ SEQUENCE 329 AA; 37613 MW; 7018702DC24C4A2 CRC64;

Query Match 72.5%; Score 1629; DB 11; Length 329;
 Best Local Similarity 92.1%; Pred. No. 2.4e-130; Matches 303; Conservative 17; Mismatches 9; Indels 0; Gaps 0;
 Qy 96 MNOVLDIAYENKPKPYLYGRGSSSEAMVEGHIPFIFTKWLQDVENVPLVQMTDEKEYL 155
 Db 1 MNQILDAYENKPKPYLYGRGSSSEAMVEGHIPFIFTKWLQDVENVPLVQMTDEKEYL 60

Qy 156 WMDLTQDQAYGAVENAKDLIAGEDTINKTFPSDLYMGSISGFYKVWIKQKHTFNO 215
 Db 61 WMDLTQDQAYGAVENAKDLIAGEDTINKTFPSDLYMGSISGFYKVWIKQKHTFNO 120

Qy 216 VKGIFGFTSDQIGKSFPAQAPSNSFQIFRDTQICLPCAIQDPYFMRD 275
 Db 121 VKGIFGFTSDQIGKSFPAQAPSNSFQIFRDTQICLPCAIQDPYFMRD 180

Db 181 VAPRIGHKPALKHSTFPALQAGAQTMNASPNNSTPLTDQAKQIKTKVNHAFSGRD 335
 Qy 336 TEERHOPGGNGNDVDFRMVLPFLIEDDKLQIRKQTYSGMLTGILKKKALEVQPLI 395
 Db 241 TVEEHOPGGNGNDVDFRMVLPFLIEDDKLQIRKQTYSGMLTGILKKKALEVQPLI 300

Qy 396 AEHQARRKEVTEBIVKESWTPPKLKFDEQ 424
 Db 301 AEHQARRKEVTEBIVKESWTPPKLKFDEQ 329

RESULT 4

070184 PRELIMINARY; PRT; 305 AA.

ID 070184; PRELIMINARY; PRT; 305 AA.

AC 070184; PRELIMINARY; PRT; 305 AA.

DT 01-AUG-1998 (TREMBREL_07, Created)

DT 01-AUG-1998 (TREMBREL_07, Last sequence update)

DT 01-MAR-2002 (TREMBREL_20, Last annotation update)

DE TRYPTOPHANT-tRNA synthetase (Fragment).

OS Cavia porcellus (Guinea pig).

OC Bokarwota; Metacoda; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

RN STRAIN=HARTORY; TISSUE=SPLEEN; Mammalia; Bokarwota; Rodentia; Hystricognathi; Caviidae; Cavia.

RN [1] SEQUENCE FROM N.A.

RN Yang D.; Goto R.; Watanabe N.; Kobayashi Y.; Identification and Cloning of Genes Whose Expressions are Elevated during DNCB-induced Guinea Pig Skin Delayed-type Hypersensitivity Reaction."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

RN EMBL; AB012222; BAB25288.1; -.

DR InterPro; IPR002305; tRNA-synt_1b.

DR InterPro; IPR002306; Trp_tRNA-synt_1b.

DR PRINTS; PRO1039; TRNA-SYNTTRP.

DR PR00579; tRNA-synt_1b; 1.

DR PRINTS; PR01039; TRNA-SYNTTRP.

DR Aminoacyl-tRNA synthetase.

FT NON_TER 1

SQ SEQUENCE 305 AA; 34838 MW; 0937164333780BB7 CRC64;

Query Match 68.4%; Score 1537; DB 11; Length 305;
 Best Local Similarity 94.4%; Pred. No. 1.4e-122; Matches 288; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 120 EAMHVUHLIPIFKWLQDVENVPLVQMTDEKEYLTLDDQAYGDAVENAKOTIAG 179
 Db 1 EAMHVUHLIPIFKWLQDVENVPLVQMTDEKEYLTLDDQAYGDAVENAKOTIAG 60

Qy 180 FDINKTPFISDLYMGSISGFYKVWIKQKHTFNOVKGIFGFTSDCGKISPA1QA 239
 Db 61 FDINKTPFISDLYMGSISGFYKVWIKQKHTFNOVKGIFGFTSDCGKISPAVOAA 120

Qy 240 PSPSNASPQFRDRDIOCLPCAIQDPYFMRD 299
 Db 121 PSFSNASPQIFRDTIQCLPCAIQDPYFMRD 180

Qy 300 QTMSASDPNSIIFLTDQAKQIKTKVNHAFSGRD 359
 Db 181 QTMSASDPNSIIFLTDQAKQIKTKVNHAFSGRD 240

Qy 360 LEPPDKLQEIRKDYTSGMLTGELKKKALEVQPLIAEHRKEVTDVKEFMPYRKL 419
 Db 241 LEPPDKLQEIRKDYTSGMLTGELKKKALEVQPLIAEHRKEVTDVKEFMPYRKL 300

Qy 420 SFDFQ 424
 Db 301 SFHFQ 305

RESULT 5

O9U4Y1 PRELIMINARY; PRT; 430 AA.

ID O9U4Y1; PRELIMINARY; PRT; 430 AA.

AC O9U4Y1; PRELIMINARY; PRT; 430 AA.

DT 01-MAY-2000 (T-EMBREL_13, Created)

DT 01-MAY-2000 (T-EMBREL_13, Last sequence update)

DT 01-JUN-2002 (T-EMBREL_21, Last annotation update)

DE Tryptophanyl-tRNA synthetase (AT21437P).

GN ATTS-TRP OR CG9135.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Pterygota; Neoptera; Endopterygota; Drosophilidae; Drosophila; Hydrodioidae; Drosophilidae; Drosophila; Ox NCBI_TaxID=7227;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=99250164; PubMed=10233165;

RA Seshaiah P.; Andrew D.J.; RT "WRS-855: A tryptophanyl-tRNA synthetase expressed to high levels in the developing Drosophila balvany gland."; Mol. Biol. Cell 10:1595-1608(1999).

RN SEQUENCE FROM N.A.

RA Stapleton M.; Brookstein P.; Hong L.; Agbayani A.; Carlson J.; Champre M.; Chavez C.; Dorsett V.; Dresnok D.; Farfan D.; Frise E.; George R.; Gonzalez M.; Guarin H.; Kronmiller B.; Li P.; Liao G.; Miranda A.; Mongall C.J.; Munro J.; Pacleb J.; Paragas V.; Park S.; Patel S.; Phouanavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.; Celniker S.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RA EMBL; AB122156; AF20166.1; -.

DR EMBL; AY05249; AAL69116.1; -.

DR FlyBase; FEGn0010803; Aab-trp.

DR InterPro; IPR002305; tRNA-synt_1b.

DR InterPro; IPR001412; tRNA-synt_1.

DR InterPro; IPR002306; Trp_tRNA-synt_1b.

DR Pfam; PF00579; tRNA-synt_1b; 1.

DR PRINTS; PRO1039; TRNA-SYNTTRP.

	DR	TIGRFAMs; TIGR00233; tRPS; 1.	NON TER.	1
	DR	PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.	SQ	SEQUENCE 420 AA; 46975 MW; 4AF7088AF426AEB6 CRC64;
KW		Aminoacyl-tRNA synthetase.		
SQ		SBQUNCE 430 AA; 47985 MW; 2E3F9E9BC1E9979A CRC64;		
Query Match		Best Local Similarity 61.5%; Score 1382; DB 5; Length 430; Matches 263; Conservative 63; Mismatches 85; Indels 16; Gaps 3;		
DR		Best Local Similarity 61.6%; Pred. No. 3.6e-109; Matches 263; Conservative 63; Mismatches 85; Indels 1; Gaps 1;		
QY		10 DYKADCPGPNAPTSNNGDPA-----TEAE-----EDNDPWTQVTSSAKGIDYD 54	QY	12 KADCPGPNAPTSNNGDPA-----TEAE-----EDNDPWTQVTSSAKGIDYD 54
Db		3 DTETEVVGVATLNGPDAPEVETGDAQEGATAPETDVDPWNVASSNDAGYD 62	Db	10 KEPDEPEVGTGDAQEGATAPETDVDPWNVASSNDAGYD 62
QY		55 KLVTRFGSSKIDKELINRERATCOPRHFLRGIFFSRHMNNOVLDAYENKCFPYLTG 114	QY	72 RERATGCRPHFLRGIFFSRHMNNOVLDAYENKCFPYLTG 114
Db		63 KLIKRFGGSKIDDELLARPEKKITOKPAHFFIRROMPFSHRDILHTREQSKPFLYTG 122	Db	70 RERATGCRPHFLRGIFFSRHMNNOVLDAYENKCFPYLTG 122
QY		115 RIGSSEAMEHVGHLIPFLIKWLODVENPLVTOIMTDDKXWKLTLQAYSDAVENAKD 174	QY	132 FTKLQLDFVNVLVIQMTDDEKYLWKLTLQAYSDAVENAKDIIACGFDINKTFPSDL 191
Db		123 RGPSSGLHVGHLPVPTMVKWLOPFTDVLVLIOTDDEKTLWKLQDAIKLGRENAKD 182	Db	130 MTKMQLEPFTDVLVLIOTDDEKTLWKLQDAIKLGRENAKDIAVGFDNKTFPSDL 189
QY		175 ILAGFDINKTFPSDLQYNGMSGFVKVVKCOKHVTFNQVKIGFTDSOCIGKSF 234	QY	192 DWGMSSCFSYKVNVKQCHVTFNQVKIGFTDSOCIGKSF 251
Db		183 IVAIGFDINKTFPSNLBVGKCPAMOYILOKCVTENQVKIGFTDSOCIGKSF 242	Db	190 EFGKCPAMOYILOKCVTENQVKIGFTDSOCIGKSF 249
QY		235 AIQAPSFSNSPFOIPLRDTDIOCLICPAIDQDPYFRMRDVARPIGYKPALLHSTFP 294	QY	252 DRDIOCIPCAIDQDPYFRMRDVARPIGYKPALLHSTFPALOGAKTRMSASDPSN 311
Db		243 AQAQAPAISSTFPIFGNR-KVHCLIPCAIDQDPYFRMRDVARPIGYKPALLHSTFP 301	Db	250 NR-KVHCLIPCAIDQDPYFRMRDVARPIGYKPALLHSTFPALOGAKTRMSASDPSN 308
QY		295 ALGAQTRNSASISPNSITLTDYKOIKVVKHAFSGGRDTIEHHRQGGNCVDVSMULTELEDDKQIRK 354	QY	312 IFITDTAKQIKVVKHAFSGGRDTIEHHRQGGNCVDVSMULTELEDDKQIRK 371
Db		302 ALQGAKTMSASDONSAYVLTDPKQIKVVKHAFSGGRDTIEHHRQGGNCVDVSMULTELEDDKQIRK 361	Db	309 VYLTDTPOIQIKVVKHAFSGGRDTIEHHRQGGNCVDVSMULTELEDDKQIRK 368
QY		355 YLTTFPLEDDKQIKVVKHAFSGGRDTIEHHRQGGNCVDVSMULTELEDDKQIRK 414	QY	372 DYTSGAMITGEKKALKALEVOLPLIAEHARRKEVTDIVKVERMPTRKSF 421
Db		362 LKQFLEDDAKLKEVRAVSKGENITGEKKALKALEVOLPLIAEHARRKEVTDIVKVERMPTRKSF 421	Db	369 AVSKGENITGEKKALKALEVOLPLIAEHARRKEVTDIVKVERMPTRKSF 418
QY		415 TPKLUSF 421		
Db		422 EURPLKF 428		
RESULT 6				
ID	Q9U4Y0	PRELIMINARY; PRT; 420 AA.		
AC	Q9U4Y0;			
DT	01-MAY-2000 (TREMBlre. 13, Created)			
DT	01-MAY-2000 (TREMBlre. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBlre. 21, Last annotation update)			
DE	TRYPTOPHYL-tRNA synthetase (Fragment).			
GN	RATS-TRP OR CG9735.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Diptera; Brachycera; Muscomorpha; Embryodea; Drosophilidae; Drosophila.			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Embryodea; Drosophilidae; Drosophila.			
OC	OC			
OX	OX			
RESULT 7				
ID	Q9VHG2	PRELIMINARY; PRT; 430 AA.		
AC	Q9VHG2;			
DT	01-MAY-2000 (TREMBlre. 13, Created)			
DT	01-MAY-2000 (TREMBlre. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBlre. 21, Last annotation update)			
DE	Ats-TSP protein.			
GN	Atts-TSP OR CG9735.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Diptera; Brachycera; Muscomorpha; Embryodea; Drosophilidae; Drosophila.			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Embryodea; Drosophilidae; Drosophila.			
OC	OC			
RN	RN [1]			
RP	SEQUENCE FROM N_A.			
RC	RC STRAIN-BERKELEY; MEDLINE=20196006; PubMed=10731132;			
RC	RC Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Boyle C., Baxter E.G., Heitk G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burris K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cisneros S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M., Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferrer S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitt A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPheron D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J.J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskeen D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purk V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003682; AAC2236.1; --.
 DR PRINTS; PR01039; TRNA-SYNT_1B.
 DR InterPro; IPR002305; tRNA-synt_1B.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002306; TRP_tRNA-synt_1B.
 DR Pfam; PF00079; tRNA-synt_1B; 1.
 DR PRINTS; PR01039; TRNA-SYNT_1B.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR SEQUENCE; P430 AA; 47971 MW; 2938EEBCC9E979F CRC64;
 Query Match 61.4%; Score 1378; DB 5; Length 430;
 Best Local Similarity 61.4%; Pred. No. 7.8e-109;
 Matches 262; Conservative 64; Mismatchs 85; Indels 16; Gaps 3;
 QY 10 DYKADCPGPNPAPTSNHOPDA-----TEAE-----EDFVDPWTQTSAGKIDYD 54
 Db 3 DPKETKVTEGVVEALTLNGRPDKAPVETGTDQAQEGATAPTEVQDPPNVAASNDAGYD 62
 QY 55 KJIVVRFGSSSKIDKEKLINRERATGQRPHFLFRGIGFSHHRDMQNQVDAHENRCPFLYTG 114
 Db 63 KLUKRFGSSSKIDBELIARFEKTGKPAHNFIRGMFFSHRDQHTILTREQQKPFPLYTG 122
 QY 115 RGPSSRAMEHVGHLIPRFTKWDQDVENPVLQMTDDEKVKMDITDQAVGDAVENAKD 174
 Db 123 RGPSSRAMEHVGHLIPRFTKWDQDVENPVLQMTDDEKVKMDITDQAVGDAVENAKD 182
 QY 175 IIACGFQDINKTIFSDDLYMGMSGFVKNVKIQKHTFPNQKGIFGFTSDCIGKISFP 234
 Db 183 IVAIGEFDNKTFIINNLIEFVGKCPAMVNITIQLCVTFNQKGICRGFDSDIIGKIGP 242
 QY 235 AJQAPSFSNSPQIPIRDRDIOCLPCAIDDPPYFMRTRDAPRIGYPKPMLHSTFP 294
 Db 243 AJQAPSFSNSPQIPIRDRDIOCLPCAIDDPPYFMRTRDAPRIGYPKPMLHSTFP 301
 QY 295 AAGGAOTKNSASDPNSIPLTTAQKQTKVVKHASSGGDRTTEERQFGNCVDVUFM 354
 Db 302 AAGQAKTMSASDQNSAVYLTDIPOKTKNKKYAFSGGRVSVBEEHKLGGPEVDVSYQ 361
 QY 355 YITFLEDDDKQEIQRKDUTQSAMLTSBLKKALIEVQPLIAHQARKETTEIVKEM 414
 Db 362 LIKFFLEDDAKLKEEVRYAVSKEMLTGBIKKAVETLTPIVEQHQARKLITDEVLDKF 421
 QY 415 TPRLSLF 421
 Db 422 EURLPKF 428

RESULT 8

Q9SR15 PRELIMINARY; PRT; 402 AA.

ID 09SR15 AC 09SR15; DT 01-MAY-2000 (TREMBREL. 13, Created) DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)

DR 01-JUN-2002 (TREMBREL. 21, Last annotation update)
 DE Putative tryptophanyl-tRNA synthetase.
 GN F7O18_7 OR AT3G4600.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Bakaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophyta;
 OC Streptophytina; Magnoliophytina; Eudicotyledopsida; Core eudicots; Rosidae;
 OC Eurosididae II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1] NCBI_TAXID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F7O18 genomic sequence.";
 RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Natsumeka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinm P., Southwick A., Shinomaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Arabidopsis Full Length cDNA Clones.";
 DR Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AAC01437; AAF04890_1; --.
 DR InterPro; IPR002305; tRNA-synt_1B.
 DR RLU; AY080709; AAB5027_1; --.
 DR InterPro; IPR001412; tRNA-SYNT_1.
 DR InterPro; IPR002306; TRP_tRNA-synt_1B.
 DR Pfam; PF00079; tRNA-synt_1B; 1.
 DR PRINTS; PR01039; TRNA-SYNT_1B.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR TIGR00233; trps; 1.
 DR SEQUENCE; P402 AA; 45754 MW; B9BEA75EB5D6CD15 CRC64;
 SQ Aminoacyl-tRNA Synthetase.
 Query Match 57.9%; Score 1301; DB 10; Length 402;
 Best Local Similarity 60.3%; Pred. No. 2.5e-102;
 Matches 240; Conservative 66; Mismatches 88; Indels 4; Gaps 2;
 QY 29 DATEAE--EDFVDPWTQTSAGKIDYDJKLVFVFGSSSKIDKEKLINRERATGQRPHFLR 86
 Db 7 DEREASSESEQVNPMEVASAKGGKIDYDJKLIDKFGQRLIDESLDRVQLRTSRQPHFLR 66
 QY 87 RGIFESSHRDMQVQDLYENKRPFLYTGCRPSSEAHVGHLIPRFTKWDQDVENPVL 146
 Db 67 RSVFFFAHRDFNBILDAVERGDKFPLYTGCRPSSEAHVGHLIPRFTKWDQDVENPVL 126
 QY 147 QMTDDEKVLKDILTDQAGDAVENAKDIIACGFQDINKTIFSDDLYMGMSGFVKNVK 206
 Db 127 OLTDDEKSIIWNLVSVERSQRAENAKDIIACGFQDINKTIFSDDLYMGMSGFVKNVK 184
 QY 207 IOKHVTFNQVKGIGFTSDCIGKISFPATOAPSFSNSPQIPIRDRDIOCLPCAIDD 266
 Db 185 VPKCVTLANKAMIGFGSGEDFIAKLSFPVQAVPSPSFSPHFLFOKDNURCLFCIAID 244
 QY 267 DPYFRMTRDAPRIGYPKPMLHSTFPAGQAGTMSASDPNSIPLTTAQKQTKV 326
 Db 245 DPYFRMTRDAPRIGYPKPMLHSTFPAGQAGTMSASDPNSIPLTTAQKQTKV 304
 QY 327 KHAFSGGRTDEERQFGNGCVDYDFMFYTFLEDDDKQEIQRKDUTQSAMLTSBLK 386
 Db 305 RYAFSGQDSKTEKHLGALBEVDIYVQKYSRFLDESELEHKIGYGSRMUIGEVK 364
 QY 387 LIBVQPLIAHQARKEVDEIVKEMPTKLSDFQ 424
 Db 365 LTEVLTIEVERHRARRAAVTDDEMUDAFMAVRPLPSME 402

RESULT 9

Q9UIR2 PRELIMINARY; PRT; 324 AA.
 ID Q9UIR2
 AC Q9UIR2;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 20, Last annotation update)
 DE Y00D3A.1 protein.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabdiidae; Peloderinae; Caenorhabditis.
 RN [1] NCBI_TaxID=6239;
 RN [2] Sequence FROM N.A.
 RP SSEQUENCE FROM N.A.
 RA Harris B.R.;
 RL Submitted (SBP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SSEQUENCE FROM N.A.
 RA MEDLINE=99069613; PubMed=9851916;
 RT "genome sequence of the nematode *C.elegans*: A platform for investigating biology.";
 RL Science 282(2012):1918(1998).
 DR EMBL; AL13253;
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR002306; tRNAsynt_1b.
 DR PRINTS; PR01039; TRANASNTHTRP.
 DR SEQUENCE 324 AA; 36289 MW; 6E687E6E420ECC12 CRC64;
 Query Match 45.7%; Score 1027; DB 5; Length 324;
 Best Local Similarity 64.9%; Pred. No. 3; 8e-79;
 Matches 194; Conservative 39; Mismatches 64; Indels 2; Gaps 1;
 OY 27 GPDATSEEDFVDPWTVOTSSAKIDYKUINVARGGSKSKIDELNRERATGQRPHFLR 86
 Db 23 GGSVOQEDBEDRVPWTVOTSSAKIDYKUINVARGGSKSKIDELNRERATGQRPHFLR 86
 OY 87 RGIFPFSHRMNQVDAVENKKPFVLYTERGRGPSSRAMHYGHLLIPITFKMLQDVNVPLI 146
 Db 83 RGMFPAHARDLTAILDRKEOGKPPFLYTGRGASSCSLHLGLHVPIFTKWLQEVFDVPLI 142
 OY 147 QMDDEKYLWKLDTLQAVGDAVENAKDIACTPDINKTFSLDYGMGMSFYKVVK 206
 Db 143 QMTDDEKPLWKDMKDVDEAKMARENMDITISVGDPKTPFENPKD--MCPFPYENIK 200
 OY 207 IOKEVTFNOVKGIGKGFDTDSCIGKISPAIQAPSFSNSFPQIFDRDPTIOCIPICAIQ 266
 Db 201 IWKVQNTNQARAFIAGFGTBEDCIGKAAPAVAAAPCFPASSEFPQIFGRKNDIPCLPCADQ 260
 OY 267 DPYFRMRTRDVAAPRTGYPKPALLHSTFPALQGQTKMSASDPNSISIIFTDTAQIKTKV 325
 Db 261 DPFPRMRTRDVAAPRLKASKPSLIFSTFLPALTGQTKMSASEPNCIFLSDTAQIKNKV 319
 RESULT 10
 O8SQY5 PRELIMINARY; PRT; 385 AA.
 ID O8SQY5
 AC O8SQY5;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE TRYPTOPHANYL tRNA synthetase.
 GN ECU11_0530.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1] STRAIN=GB-ML;
 RP SSEQUENCE FROM N.A.
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SSEQUENCE FROM N.A.
 RA Best Local Similarity 45.9%; Pred. No. 5; 6e-62;
 Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;
 OY 385 AA; 44188 MW; 2865C3AC95PCC859 CRC64;
 Query Match 41.9%; Score 942; DB 5; Length 385;
 Best Local Similarity 46.1%; Pred. No. 8; 3e-72;
 Matches 179; Conservative 76; Mismatches 123; Indels 10; Gaps 3;
 OY 35 EDFVDPWTVOTSSAK---GIDYKLUWRFESSKIDELNRERATGQRPHFLRGGIF 90
 Db 3 EQRITPMDWVNUSTDEVPAVIDYDKLNQFGCEBKFNQALADRLEKULSGKPAHFRKGIV 62
 OY 91 FSHRDMDQVLDAYENKPFVLYTGRGSSSEAMHGHLIPIFTKWLQDVNUPLVQMTD 150
 Db 63 FAIRDENULLDETAANNPFYLTGRGSSKTMIGHTFLQKYMQDAFKRLVQIT 122
 OY 151 DEKYLWKLDTLQAVGDAVENAKDIACTPDINKTFSLDYGMGSSGYKVVKQKH 210
 Db 123 DEKFELWKSMLIEDAMAVGRENKIDVALGFDKLTVFISNVE--ASHHFSENIKIST 179
 OY 211 VTNENQVKGIGFDFSDIGKISRFPATQAPSFSNSFFQIFRQRTDQCLPRAIDOPPF 270
 Db 180 INNLNEAIKVGFDFWMSNQIYGQVERPAKBAIACPFCSSSFRRIGK--GAMCLVPAVDQDPFF 236
 OY 271 RMRDVAARRIGPKPAHLHSTFPALQGQTONMSASPNNSISIIFTDPAQKQTKVNKA 330
 Db 237 RLARDKQAKALGERKPSIYVSLPDKVKNRNSASDPPNSIYLLDDQDTTRKKIAYA 296
 OY 331 SGGRDTEBFRHFGGNCDVDSFMYLTFPLEDDDKLEQIRKDVTSGAMLTGELKALLEV 390
 Db 297 SGCRKTLEBREKKGDDVDPVPEYLVFLDDQEELEYKRSYIKGBTSKEMKEKCVV 356
 OY 391 LQPLIAEBQARKEVTDIYKGFMTPRK 418
 Db 357 IQSFVSRVQESRKRVTDLDRAPIDINK 384
 RESULT 11
 OQ453 PRELIMINARY; PRT; 385 AA.
 ID OQ453
 AC OQ453;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE TRYPTOPHANYL-tRNA synthetase.
 GN PR0241.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 RN [1] SSEQUENCE FROM N.A.
 RC STRAIN=VCL / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "the complete sequence of the Pyrococcus furiosus genome";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE01049; HAL0365.1;
 KW Aminosacyl-tRNA synthetase; Complete proteome.
 SQ SSEQUENCE 385 AA; 45178 MW; 3A7A628958200CCC CRC64;
 Query Match 36.8%; Score 826.5; DB 17; Length 385;
 Best Local Similarity 45.9%; Pred. No. 5; 6e-62;
 Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;

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OM protein - protein search, using sw model

Run on: July 10, 2003, 12:27:20 ; Search time 27.2194 Seconds
 (without alignments)
 3035.516 Million cell updates/sec

Title: US-009-813-718-10_COPY_71_471

Perfect score: 2116

Scoring table: BIOSIM62

Sequence: 1 SNIGPDATEAEEDVDPWIV.....VTDRLIVKFERMTRKUSDFDQ 401

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTRMBBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1957	92.5	475	11 Q9DC65	Q9dc65 mus musculu
2	1957	92.5	481	11 Q9PJ58	Q9pj58 mus musculu
3	1629	77.0	329	11 Q9dR99	Q9dr99 mus musculu
4	1537	72.6	305	11 Q9t084	cavia porce
5	1374.5	65.0	420	5 Q9UY00	Q9uy00 drosophila
6	1374.5	65.0	420	5 Q9AY11	Q9ay11 drosophila
7	1370.5	64.8	430	5 Q9WFG2	Q9wfg2 drosophila
8	1301	61.5	402	10 Q9RS15	Q9rs15 arabidopsis
9	1027	48.5	324	5 Q9UR2	Q9ur2 caenorhabditis
10	942	44.5	385	5 Q9SY05	Q9sy05 encephalito
11	826.5	39.1	385	17 Q8U453	Q8u453 pyrococcus
12	826.5	39.1	385	5 Q9U1F5	Q9u1f5 leishmania
13	682	32.2	136	6 Q95295	Q95295 sub scrofa
14	453	21.4	374	17 Q8TYF7	Q8tyf7 methanopyru
15	329.5	15.6	430	5 Q8TU71	Q8tu71 methanopyru
16	310	14.7	111	5 Q95118	Q9y18 encephalito

ALIGNMENTS

RESULT 1

ID	Q9DC65	PRELIMINARY;	PRT;	475 AA.
AC	Q9DC65;	DT 01-JUN-2001 (TREMBLrel. 17, Created)	DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DE		DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE		DE Adult male lung cDNA, RIKEN full-length enriched library, clone-1200002C07, full insert sequence.		
GN		GN MARS.		
OS		OS Mus musculus (Mouse).		
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC		OC NCBI_TaxID:10090;		
RN	[1]	RN		
RP		RP SEQUENCE FROM N.A.		
RC		RC STRAIN=C57BL/6J; TISSUE=LUNG;		
RX		RX MEDLINE=21085660; PubMed=1211851;		
RA		RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiysawa H., Kondo S., Yamanka I., Saito T., Okazaki H., Gotohori T., Bono H., Kasukawa T., Saito R., RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Straubli S., Suzuki R., Tomita M., Wagner L., Washio T., RA Sekai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G., RA Browne J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Butz C., Fletcher C., Fujita M., Garibaldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oaka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsukii S., RA Hayashizaki Y.; RT "Functional annotation of a full-length mouse cDNA collection."; RT DR ENSEMBL: AK005451; BAB23357.1; -.		

DR MGD; MGJ:104630; Wars.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002306; tRNA-synt_1b.
 DR InterPro; IPR000738; WHEP-TRS.
 DR Pfam; PF00519; tRNA-synt_1b; 1.
 DR Pfam; PF00438; WHEP-TRS; 1.
 DR PRINTS; PR01039; TRNAsynthRP.
 DR TIGRFAM; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP-TRS; 1.
 DR Aminoacyl-tRNA_Synthetase.
 DR SEQUENCE; 475 AA; 54325 MW; A754E1DDF58E2EF3 CRC64;
 DR SEQUENCE; 475 AA; 53541 MW; C3467FFB85521DE4C CRC64;

Query Match 92.5%; Score 1957; DB 11; Length 475;
 Best Local Similarity 91.5%; Pred. No. 3.7e-159;
 Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 NHGPDATTAEEFDVDPWTQTSAGKIDYDLYKLIVREGSSKIDELINIRATGQRPHF 61
 Db 76 NCDSDATKASEDFDVDPWTQTSAGKIDYDLYKLIVREGSSKIDELINIRATGQRPHF 135
 QY 62 LRRGIFFSHRDNQIQLDAVENKPKFYLTGRGSSEAMVGHLPFTKIQDVFENPL 121
 Db 136 LRRGIFFSHRDNQIQLDAVENKPKFYLTGRGSSEAMVGHLPFTKIQDVFENPL 195
 QY 122 VQMTDDEKYLWQDLTDQAYGDAVENAKDITACGFINKTFRSDIDYMGMSGTYKV 181
 Db 196 VIQMSDDEKYLWQDLTQAYGDAVENAKDITACGFINKTFRSDIDYMGMSGTYKV 255
 Db 182 VKIQLKHTFNOVKGIGFTSDCIGKSFPAQAAFSNSFPQIERTDQCLICAI 241
 256 VKIQLKHTFNOVKGIGFTSDCIGKSFPAQAAFSNSFPQIERTDQCLICAI 315
 QY 242 DQPYFRMTRDVARIGPKPALHSTPPALQAOQTMSASPNSFLDTAKOIKT 301
 Db 316 DQPYFRMTRDVARIGPKPALHSTPPALQAOQTMSASPNSFLDTAKOIKSK 375
 QY 362 KALIEVQPLIAHQARKEVTEIVKEMTPRKLSFDFQ 401
 302 VNGHAFGSGRDTTEHHROFGGNCDVDSFMVLTFFLEDDDKLQEIRKDYTSGAMLTCBLK 361
 Db 376 VNGHAFGSGRDTTEHHROFGGNCEVDVSMVLTFFLEDDDKLQEIRKDYTSGAMLTCBLK 435
 436 KULIDVLOPLIAHQARKEVTEIVKEMTPRKLSFDFQ 475

RESULT 2
 Q99J5B
 ID Q99J5B PRELIMINARY; PRT; 481 AA.
 AC Q99J5B; 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE TRYTOPHANYL-tRNA synthetase.
 GN WARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_MaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RK MEDLINE=21085660; PubMed=1121851;
 RA Kawai J., Shingawa K., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Mizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
 RA Saito T., Okazaki Y., Gotobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalow S., Cassavant T.,
 RA Pleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsu Y., Nikaido T., Pelese G., Quackenbush J.,
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boefelli D., Boujunga N., Carninci P., de Bonalio M.F.,
 RA Brownstein M.J., Bult C., Flecher C., Fujita M., Garibaldi M.,
 RA Gustincovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaferri J., Montaress P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 DR PRINTS; PR01039; TRNAsynthRP.

DR TIGRFAM; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP-TRS; 1.
 DR Aminoacyl-tRNA_Synthetase.
 DR SEQUENCE; 481 AA; 54325 MW; A754E1DDF58E2EF3 CRC64;
 DR SEQUENCE; 481 AA; 53541 MW; C3467FFB85521DE4C CRC64;

Query Match 92.5%; Score 1957; DB 11; Length 481;
 Best Local Similarity 91.5%; Pred. No. 3.7e-159;
 Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 NHGPDATTAEEFDVDPWTQTSAGKIDYDLYKLIVREGSSKIDELINIRATGQRPHF 61
 Db 76 NCDSDATKASEDFDVDPWTQTSAGKIDYDLYKLIVREGSSKIDELINIRATGQRPHF 135
 QY 62 LRRGIFFSHRDNQIQLDAVENKPKFYLTGRGSSEAMVGHLPFTKIQDVFENPL 121
 Db 136 LRRGIFFSHRDNQIQLDAVENKPKFYLTGRGSSEAMVGHLPFTKIQDVFENPL 195
 QY 122 VQMTDDEKYLWQDLTDQAYGDAVENAKDITACGFINKTFRSDIDYMGMSGTYKV 181
 Db 196 VIQMSDDEKYLWQDLTQAYGDAVENAKDITACGFINKTFRSDIDYMGMSGTYKV 255
 QY 182 VKIQLKHTFNOVKGIGFTSDCIGKSFPAQAAFSNSFPQIERTDQCLICAI 241
 256 VKIQLKHTFNOVKGIGFTSDCIGKSFPAQAAFSNSFPQIERTDQCLICAI 315
 QY 242 DQPYFRMTRDVARIGPKPALHSTPPALQAOQTMSASPNSFLDTAKOIKT 301
 Db 316 DQPYFRMTRDVARIGPKPALHSTPPALQAOQTMSASPNSFLDTAKOIKSK 375
 QY 362 KALIEVQPLIAHQARKEVTEIVKEMTPRKLSFDFQ 401
 Db 436 KULIDVLOPLIAHQARKEVTEIVKEMTPRKLSFDFQ 475

RESULT 3
 Q99J89
 ID Q99J89 PRELIMINARY; PRT; 329 AA.
 AC Q99J89; 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE TRYTOPHANYL-tRNA synthetase.
 GN WARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RK MEDLINE=21085660; PubMed=1121851;
 RA Kawai J., Shingawa K., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Mizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
 RA Saito T., Okazaki Y., Gotobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalow S., Cassavant T.,
 RA Pleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsu Y., Nikaido T., Pelese G., Quackenbush J.,
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boefelli D., Boujunga N., Carninci P., de Bonalio M.F.,
 RA Brownstein M.J., Bult C., Flecher C., Fujita M., Garibaldi M.,
 RA Gustincovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaferri J., Montaress P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 DR PRINTS; PR01039; TRNAsynthRP.

RA	RT	Hayashizaki Y.; Functional annotation of a full-length mouse cDNA collection.";	Matches
RL	Nature 409:685-690(2001); EMBL; AK007754; BAB25235.1; -.	97 EAMVGHLLPFIFTKWLQDVFNPNVLVQIOMTDEKKILWKOITDLOQYDAVENAKOIIACG	Qy
DR	MGD; MG1:04630; Wars.	1 EAMVGHLLPFIFTKWLQDVFNPNVLVQIOMTDEKKILWKOITDLOQYDAVENAKOIIACG	Db
DR	InterPro; IPR002305; tRNA-synt_1b.	157 FDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQVKJIGFTSDCLGKISFFAIQAA	Qy
DR	InterPro; IPR002306; Trp_tRNA-synt_1b.	60 FDNKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQVKJIGFTSDCLGKISFFAIQAA	Db
DR	Pfam; PF00579; tRNA-synt_1b; 1.	157 FDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQVKJIGFTSDCLGKISFFAIQAA	Qy
DR	PRINTS; PRO1039; TRNAsYNTHTRP.	61 FDNKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQVKJIGFTSDCLGKISFFAIQAA	Db
DR	PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.	120 FDNKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQVKJIGFTSDCLGKISFFAIQAA	Qy
SQ	SEQUENCE; 329 AA; 3761 MW; 701E02DC244C4A2 CRC64;	121 PSFSNSFPQFDRTDIOCLPCALDODPYFRMRD	Db
Query Match	Best Local Similarity 77.0%; Score 1629; DB 11; Length 329;	121 PSFSNSFPQFDRTDIOCLPCALDODPYFRMRD	Qy
Matches	Loc 303; Conservative 92.1%; Pred. No. 2.7e-131; Mismatches 9; Indels 0; Gaps 0;	121 PSFSNSFPQFDRTDIOCLPCALDODPYFRMRD	Db
Qy	73 MNQVLDAVENKPKPFYLYGRGSSSEAMEVGHLLPFIFTKWLQDVFNPNVLVQIOMTDEKKYL	132 1 MNQVLDAVENKPKPFYLYGRGSSSEAMEVGHLLPFIFTKWLQDVFNPNVLVQIOMTDEKKYL	Qy
Db	1 WKLDTDOAYGAVENAKOIIACGFDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQ	60 1 WKLDTDOAYGAVENAKOIIACGFDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQ	Db
Qy	133 WKLDTDOAYGAVENAKOIIACGFDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQ	192 61 WKLDTDOAQSIVTENAKOIIACGFDINKTFISDDLYNGMSSGFYKVNVKIQKHTFVNQ	Qy
Db	193 VRGIFGFGFDSDCGKTSPPAQAPSFNSFPQFDRTDIOCLPCALDODPYFRMRD	252 193 VRGIFGFGFDSDCGKTSPPAQAPSFNSFPQFDRTDIOCLPCALDODPYFRMRD	Db
Db	121 VKGIFGFTDSCLGKTSPPAQAPSFNSFPQFDRTDIOCLPCALDODPYFRMRD	180 121 VKGIFGFTDSCLGKTSPPAQAPSFNSFPQFDRTDIOCLPCALDODPYFRMRD	Qy
Qy	253 VAPRIGPKPAHLHSTFPALQAGQTMASADNSISFLTDIAKQIKUKUNKHAFSGRD	312 181 VAPRIGPKPAHLHSTFPALQAGQTMASADNSISFLTDIAKQIKUKUNKHAFSGRD	Qy
Db	181 VAPRIGPKPAHLHSTFPALQAGQTMASADNSISFLTDIAKQIKUKUNKHAFSGRD	240 181 VAPRIGPKPAHLHSTFPALQAGQTMASADNSISFLTDIAKQIKUKUNKHAFSGRD	Db
Qy	313 TIEBHRQFGNCDDVNSPMULTFLEDDDKLEQIRKDVTSGAMLTGEKKALTEVLOQPLI	372 313 TIEBHRQFGNCDDVNSPMULTFLEDDDKLEQIRKDVTSGAMLTGEKKALTEVLOQPLI	Qy
Db	372 241 TVEERHQFGNCDDVNSPMULTFLEDDDKLEQIRKDVTSGAMLTGEKKALTEVLOQPLI	300 241 TVEERHQFGNCDDVNSPMULTFLEDDDKLEQIRKDVTSGAMLTGEKKALTEVLOQPLI	Db
Qy	373 AHQARKKEVETDIVEKFTPKLSPFPO	401 373 AHQARKKEVETDIVEKFTPKLSPFPO	Qy
Db	301 AHQARKKAVTETVKEMTPROLSFHQ	329 301 AHQARKKAVTETVKEMTPROLSFHQ	Db
RESULT 4			
ID	070184	PRELIMINARY; PRT; 305 AA.	Q94AY0
ID	070184;	PRELIMINARY; PRT; 305 AA.	Q94AY0
DT	01-AUG-1998 (TREMBrel. 07, Last sequence update)	01-MAY-2000 (TREMBrel. 13, Last sequence update)	DT
DT	01-AUG-1998 (TREMBrel. 07, Last annotation update)	01-MAY-2000 (TREMBrel. 13, Last annotation update)	DT
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)	01-JUN-2002 (TREMBrel. 21, Last annotation update)	DE
DB	Tryptophan-tRNA synthetase (Fragment).	Tryptophanyl-tRNA synthetase (Fragment).	GN
DB	Cavia porcellus (Guinea pig).	Drosophila melanogaster (Fruit fly).	OS
OC	Bukay-Yota; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.	OC
OC	RN [1] NCBI_TaxID=7227;	RN [1] NCBI_TaxID=7227;	OX
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	RP
RX	MEDLINE:99250164; PubMed:10233165;	MEDLINE:99250164; PubMed:10233165;	RX
RA	Seshaiyah P., Andrew D.J.;	RAT "WTS-85D: A tryptophanyl-tRNA synthetase expressed to high levels in the developing Drosophila salivary gland.";	RA
RT	01-APR-1998 (TREMBrel. 07, Last sequence update)	01-MAY-2000 (TREMBrel. 13, Last sequence update)	RT
RL	01-MAR-2002 (TREMBrel. 20, Last annotation update)	01-JUN-2002 (TREMBrel. 21, Last annotation update)	RL
DR	EMBL; AP125157; AAF20167.1; -.	EMBL; Bem0010803; Aats-trp.	DR
DR	InterPro; IPR002305; tRNA-synt_1b.	InterPro; IPR002305; tRNA-synt_1b.	DR
DR	InterPro; IPR002310; Trp_tRNA-synt_1b.	InterPro; IPR002310; Trp_tRNA-synt_1b.	DR
DR	PRINTS; PRO1039; tRNA-synt_1b; 1.	PRINTS; PRO1039; tRNA-synt_1b; 1.	DR
DR	TRIFAM; TIGR00233; trps; 1.	TRIFAM; TIGR00233; trps; 1.	DR
DR	Aminoacyl-tRNA synthetase.	Aminoacyl-tRNA synthetase.	DR
RT	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	RT
RT	STRAIN=HARTLEY; TISSUE=SPLEEN;	STRAIN=HARTLEY; TISSUE=SPLEEN;	RT
RC	Yang D., Goto R., Wakabayashi Y.; Identification and Cloning of Genes Whose Expressions are Elevated during DNGB induced Guinea Pig Skin Delayed-type Hypersensitivity Reaction.;	Identification and Cloning of Genes Whose Expressions are Elevated during DNGB induced Guinea Pig Skin Delayed-type Hypersensitivity Reaction.;	RC
RT	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.	RT
RT	NON_TER 1	NON_TER 1	RT
FT	SEQUENCE 305 AA; 34838 MW; 0937164333780EB7 CRC64;	SEQUENCE 420 AA; 46975 MW; 4AF7080AF426AEB6 CRC64;	FT
Query Match	Best Local Similarity 65.0%; Score 1374.5; DB 5; Length 420; Matches 254; Conservative 64.8%; Pred. No. 2.4e-109; Mismatches 61; Indels 1; Gaps 1;	7 ATEEAEDFDVPTQVTSKAGDVKLIVRGFSKSKIDELIARFEKICKPAHIFIRGM	Qy
FT	NON_TER 1	7 ATEEAEDFDVPTQVTSKAGDVKLIVRGFSKSKIDELIARFEKICKPAHIFIRGM	Db
FT	Aminocycl-tRNA synthetase.	7 ATEEAEDFDVPTQVTSKAGDVKLIVRGFSKSKIDELIARFEKICKPAHIFIRGM	Qy
FT	NON_TER 1	7 ATEEAEDFDVPTQVTSKAGDVKLIVRGFSKSKIDELIARFEKICKPAHIFIRGM	Db
Query Match	Score 1537; DB 11; Length 305; Pred. No. 1.8e-123;	67 FFSHRDMNQVLDAVENKPKPFYLYGRGSSGLAVGHLLPFIMTVLQDFTDPVLIQ	Qy
Best Local Similarity	94.4%;	67 FFSHRDMNQVLDAVENKPKPFYLYGRGSSGLAVGHLLPFIMTVLQDFTDPVLIQ	Db
SQ	94.4%; Pred. No. 1.8e-123;	147 FFSHRDLHILTURREQKPFYLYGRGSSGLAVGHLLPFIMTVLQDFTDPVLIQ	SQ

QY 127 DDEKYLWQLDTLQDQAQYDAVENAKDIAAGFDINKTFPSDDYMGMSGGFKNVVKIQ 186
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 148 DEEKTILWKLKDVEKAIGRENAKDIAVGFDFNKFIFNNLEFVGKCPAMQNIRIQ 207
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 187 HVTENQVKGKIGFTSDCIGKSFPAQAPSISNSPQIQRUTDQCLICAIIDPY 246
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 208 CWTENQVKGKIGFTSDCIGKSFPAQAPSISNSPQIQRUTDQCLICAIIDPY 266
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 247 FMTRDVAPRIGPKALHSTPPALQAGTMSASPNISFLTDATAKIKTKVKA 306
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 267 FMTRDVAPRIGPKALHSTPPALQAGTMSASPNISFLTDATAKIKTKVKA 326
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 307 FSGGRDTTEHHROFGGNCDVDVSFMWLTFFLEDDKLQEIRKOYTSGAMLTGBLKALIE 366
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 327 FSGGRVTTEHHRKLGVPEDVSYQOLKFELDAKLEEVRAVYSKGMLTGBLKALIE 386
|:|||:|||:|||:|||:|||:|||:|||:
QY 367 VLOPLIAHQARKEVTDIEVKEFMPTRKSF 398
|:|||:|||:|||:|||:|||:
Db 387 TLTPIVEQHQARKLITDEVLDKYFELRPLKF 418
|:|||:

RESULT 6

Q9U4YL PRELIMINARY; PRT; 430 AA.
ID Q9U4YL
AC Q9U4YL;
DT 01-MAY-2000 (TREMBrel. 13, Created)
ID 09VHG2
DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE TRYPTOPHANYL-TRNA SYNTHETASE (ATR21437P).
GN ATTS-TRP OR CG9735.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99250164; PubMed=10233165;
RA Seshaiah P., Andrew D.J.;
RT "WRS-65D: A tryptophanyl-tRNA synthetase expressed to high levels in
the developing Drosophila salivary gland.";
RL Mol. Biol. Cell 10:1595-1608(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA SPANCLETON M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champé M., Chavez C., Dorsett V., Dresnek D., Farfin D., Frisse B.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mundall C.J., Munoz J., Pacifer J., Paregas V., Park S.,
RA Patel S., Phoumanenong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Gelniker S., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP124156; AAC20166.1; -
DR EMBL: AY075249; AAL68116.1; -
DR FLYBase: FBgn000803; Aats-trp.
DR InterPro: IPR002335; tRNA-synt_1b.
DR InterPro: IPR01412; tRNA-synt_1.
DR InterPro: IPR02306; trp_tRNA-synt_1b.
DR Pfam: PF00179; tRNA-synt_1b; l.
DR PRINTS: PR0103; TRANSINTHRP.
DR TIGRFAMS: TIGR00233; trps_1.
DR PROSITE: PRO00178; AA_TRNA_LIGASE_1; 1.
DR KW Aminacyl-tRNA Synthetase
SQ SEQUENCE 430 AA; 47985 MW; 2E3FF9B9C189979A CRC64;
Matches 254; Conservative 61; Mismatches 76; Indels 1; Gaps 1;

Query Match 65.0%; Score 1374.5; DB 5; Length 430;
Best Local Similarity 64.8%; Prcd. No. 2.5e-109; T.B.C. 1;

RESULT 7

Q9VHG2 PRELIMINARY; PRT; 430 AA.
ID Q9VHG2
AC Q9VHG2;
DT 01-MAY-2000 (TREMBrel. 13, Created)
ID 09VHG2
DT 01-MAY-2000 (TREMBrel. 21, Last annotation update)
DE ATTS-TRP OR CG9735.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY; MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.-C., Blazier R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heitz G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.W., Bauw A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bentov P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borcman M.R., Bouck J., Brokstein P., Brostek P.,
RA Burts K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Douq L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara S., Fleischmann W.,
RA Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz C., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky T.A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosureti A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Mizny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzo L., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders D.R.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradlin M., Strong R., Sun E.,
RA Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,	[2]
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	SEQUENCE FROM N.A.
RA	Yeh R.-P., Zaveri J.-S., Zhan M., Zhang G., Zhao Q., Zheng L.,	RP
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	SEQUENCE FROM N.A.
RA	"The genome sequence of <i>Drosophila melanogaster</i> ,"	SEQUENCE FROM N.A.
RL	Science 287:2185-2195(2000).	SEQUENCE FROM N.A.
DR	EMBL; AE003682; AAG23136.1; -.	SEQUENCE FROM N.A.
DR	FlyBase; FBgn0010803; Aats-trp.	SEQUENCE FROM N.A.
DR	InterPro; IPR002305; tRNA-synt_1b.	SEQUENCE FROM N.A.
DR	InterPro; IPR001412; tRNA-synt_1.	SEQUENCE FROM N.A.
DR	InterPro; IPR002306; trp_tRNA-synt_1b.	SEQUENCE FROM N.A.
DR	Pfam; PF00579; tRNA-synt_1b, 1.	SEQUENCE FROM N.A.
DR	PRINTS; PRO1039; TRNA-SYNTHTRP.	SEQUENCE FROM N.A.
DR	TIGR4MS; TIGR00233; trps_1.	SEQUENCE FROM N.A.
DR	PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.	SEQUENCE FROM N.A.
DR	SEQUENCE 430 AA; 47971 MW; 293BEECC69E979F CRC64;	SEQUENCE FROM N.A.
Query	Query Match 64.8%; Score 1370.5; DB 5; Length 430;	Query Match 64.8%; Score 1370.5; DB 5; Length 430;
Matches	Best Local Similarity 64.5%; Pred. No. 5.4e-109; Mismatches 62; Indels 76; Gaps 1; Gaps 1;	Best Local Similarity 64.5%; Pred. No. 5.4e-109; Mismatches 62; Indels 76; Gaps 1; Gaps 1;
Db	7 DATEAEEDFVDPPVTQVSSAKGIDYDKULVRGSSKIDKELNRITERATGQPFRPHFRG 66	7 DATEAEEDFVDPPVTQVSSAKGIDYDKULVRGSSKIDKELNRITERATGQPFRPHFRG 66
Db	38 ATTAPEVNDPANVASSNDAGIDYDKULVRGSSKIDKELNRITERATGQPFRPHFRG 97	38 ATTAPEVNDPANVASSNDAGIDYDKULVRGSSKIDKELNRITERATGQPFRPHFRG 97
Query	67 FFSHRDMNOVQDLYAENKRPFYLTGRGPPSSRMVSHLIPITFKMQLQDVENVNPVYMT 126	67 FFSHRDMNOVQDLYAENKRPFYLTGRGPPSSRMVSHLIPITFKMQLQDVENVNPVYMT 126
Db	98 FFSHRDLHILTLREQQKPFYLTGRGPPSSRMVSHLIPITFKMQLQDVENVNPVYMT 157	98 FFSHRDLHILTLREQQKPFYLTGRGPPSSRMVSHLIPITFKMQLQDVENVNPVYMT 157
Query	127 DBDKYLUKDLTDQDAVENAQADTAGEDINKPFLPSDLDYMGMSGYKVVKIQ 186	127 DBDKYLUKDLTDQDAVENAQADTAGEDINKPFLPSDLDYMGMSGYKVVKIQ 186
Db	158 DBDEKTLMKDVEAIKLGRENADIAVGFVNUKPIFNNLEFVGKPCANTONIIRQ 217	158 DBDEKTLMKDVEAIKLGRENADIAVGFVNUKPIFNNLEFVGKPCANTONIIRQ 217
Query	187 HTFPNQVKGIRGFTSDCIGKISPPAQLQAQSFSNSFPQIIRRDTIQCILPCATDQPY 246	187 HTFPNQVKGIRGFTSDCIGKISPPAQLQAQSFSNSFPQIIRRDTIQCILPCATDQPY 246
Db	218 CTFENQVKGIRGFTGDPDKIGKGPAAQAPISSTPPICNR_KVHCLIPCAIDQPY 276	218 CTFENQVKGIRGFTGDPDKIGKGPAAQAPISSTPPICNR_KVHCLIPCAIDQPY 276
Query	247 FRMTRDVAPRIGYKPKALHSTFPALQAGQTMASDPNSNIFLDTAKOJKTCKTKNHA 306	247 FRMTRDVAPRIGYKPKALHSTFPALQAGQTMASDPNSNIFLDTAKOJKTCKTKNHA 306
Db	277 FRMTRDVAPRIGYKPKCALIHSTFPALQGAKTCKMSASDONSAYVLTDPKQIKNKINYA 336	277 FRMTRDVAPRIGYKPKCALIHSTFPALQGAKTCKMSASDONSAYVLTDPKQIKNKINYA 336
Query	307 FSGGRDTEERHQFGNCDVUSFMVLTFLDDDKLQEIRKDYTGAMTGEKLKALIE 366	307 FSGGRDTEERHQFGNCDVUSFMVLTFLDDDKLQEIRKDYTGAMTGEKLKALIE 366
Db	337 FSGGRDTEERHQFGNCDVUSFMVLTFLDDDKLQEIRKDYTGAMTGEKLKALIE 396	337 FSGGRDTEERHQFGNCDVUSFMVLTFLDDDKLQEIRKDYTGAMTGEKLKALIE 396
Query	367 VIQVPLIAHQARKEVTDIEVKEFMPRKLS 398	367 VIQVPLIAHQARKEVTDIEVKEFMPRKLS 398
Db	397 TIPTIVEQHQARKLTDDEVLDKYFSLRPLKE 428	397 TIPTIVEQHQARKLTDDEVLDKYFSLRPLKE 428
RESULT 8		
Q9SR15		
ID	09SR15 PRELIMINARY; PRT; 402 AA.	09SR15 PRELIMINARY; PRT; 402 AA.
AC	Q9SR15; [1]	Q9SR15; [1]
DT	01-MAY-2000 (TREMBLrel. 13, Created)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB	Putative tryptophanyl-tRNA synthetase.	Putative tryptophanyl-tRNA synthetase.
OS	Arabidopsis thaliana (Mouse-ear cress).	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophytina; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Eukaryota; Viridiplantae; Streptophytina; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702; [1]	NCBI_TaxID=3702; [1]
RN	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN=CV_COLUMBIA;	STRAIN=CV_COLUMBIA;
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA	Romning C.M., Koo H., Fuji C.Y., Utterback T., Barnstead M.E.,	Romning C.M., Koo H., Fuji C.Y., Utterback T., Barnstead M.E.,
RA	Bowman C.L., White O., Nieman W.C., Fraser C.M.,	Bowman C.L., White O., Nieman W.C., Fraser C.M.,
RT	"Arabidopsis thaliana chromosome III BAC F7018 genomic sequence,"	"Arabidopsis thaliana chromosome III BAC F7018 genomic sequence,"
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RESULT 9		
O9UIR2		
ID	O9UIR2 PRELIMINARY; PRT; 324 AA.	O9UIR2 PRELIMINARY; PRT; 324 AA.
AC	O9UIR2; [1]	O9UIR2; [1]
DT	01-MAY-2000 (TREMBLrel. 13, Created)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2002 (TREMBLrel. 20, Last annotation update)	01-MAY-2002 (TREMBLrel. 20, Last annotation update)
DE	Y803A.1 protein.	Y803A.1 protein.
GN	Y803A.1.	Y803A.1.
OS	Caenorhabditis elegans.	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peidorinae; Caenorhabditis.	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peidorinae; Caenorhabditis.
OX	NCBI_TaxID=6239; [1]	NCBI_TaxID=6239; [1]
RN	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RP	Harris B.R.;	Harris B.R.;
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9969613; PubMed=9951916;
 RA None;
 RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology";
 RL Science 283:2012-2018 (1998).
 DR EMBL; AL13853; CAB60139.1; -.
 DR Interpro; IPR002305; tRNA-synt_1b.
 DR Interpro; IPR002306; Trp-tRNA-synt_1b.
 DR PRINTS; PR00579; tRNA-synt_1b; 1.
 DR SEQUENCE; PR0139; tRNA-synt_1b.
 SQ 324 AA; 36289 MW; 6E687B6E420ECC12 CRC64;
 Query Match 48.5%; Score 1027; DB 5; Length 324;
 Best Local Similarity 64.9%; Pred. No. 9.6e-80;
 Matches 194; Conservative 39; Mismatches 64; Indels 2; Gaps 1;
 QY 4 GPPDAEAEEDFPDPWVQTSAGKIDYDKLVRGGSSKIDKSLINRERATCOPRHFLR 63
 DB 23 GGGVQEDBEDRVPWVETVTTGKIDYDVKLVEFGCRKLDELLARERVGCKASMLR 82
 QY 64 R3JFFSHRDMMNQTLDAYENKPKPFLYTRGLGPSEAMHGHLIPLPFIFTRKWLQDVFNVLVI 123
 . 83 R3MFAHDLTALIDRKEQGKPYLYIGRGASSGLHIGHLYPLFIFTRKWLQDVFNVLVI 142
 QY 124 QMTDDEKFILWKOMKVDDEAKMARENKMDDISVGDPTKIFIRNNFDY-MCPFPYENIVK 200
 QY 143 QMTDDEKFILWKOMKVDDEAKMARENKMDDISVGDPTKIFIRNNFDY-MCPFPYENIVK 200
 DB 184 IQKGVTEPKVKGIFGFGFDSCIGKISFPATOQAPSNSPQIFDRDTIOCLPCAIDODPYF 243
 201 IWKVNTNQARAIFGFTPDCIGKAAPCAVEAACPFASSPQIFGRKNDIPCLPCIDQ 260
 QY 244 DPYFMRMDVAPIGYPKPALHSTFPALQGQTKTNSASDNNSSITLTDMQIKIV 302
 . 261 DPFPRMTRDVAPILKASKPSLTFSTPLALTGAQTKNSASEPNTCIFLSDTAKQIKIV 319
 RESULT 10
 Q8SQY5 PRELIMINARY; PRT; 385 AA.
 ID Q8SQY5
 AC Q8SQY5;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE TRYptophanyl-TRNA synthetase.
 GN BCUL1_0530
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 RN [1] NCBI_TaxID=6035;
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-ML;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-ML;
 RX MEDLINE=2176510; PubMed=1171906;
 RA Katincka M., Duprat S., Cornilliot E., Metenier G., Thomarat F.,
 RA Presterl G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
 RA Delbac F., El Aloui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi.";
 RL Nature 414:450-453 (2001).
 DR EMBL; AL590450; CAD23963.1; -.
 SQ SEQUENCE; PR0139; 385 AA; 44188 MW; 2865C3AC95FCC859 CRC64;
 Query Match 44.5%; Score 942; DB 5; Length 385;
 Best Local Similarity 46.1%; Pred. No. 2.3e-72;
 Matches 179; Conservative 76; Mismatches 123; Indels 10; Gaps 3;

QY 12 EDPVDPWVQTSAK---GIDYDKLVRGGSSKIDKSLINRERATCOPRHFLR 67
 DB 3 EORITPDWDEVVSTDEPVPAVIDKINQFCCEKFNOQALADRIEKUSKPAHYFRRGIV 62
 QY 68 FSHRDMMQCVLAVENKPKPFLYTRGLGPSEAMHGHLIPLPFIFTRKWLQDVFNVLVI 127
 DB 63 FAHRDFNLILLDIBANNRPFVLYTRGGRPSKTMIGHTIPFLICKYMQDAFKIRLVQITD 122
 QY 128 DEKVLMQTLTDOQYQDAVENAKDIAEGEDINKPFPISLDYGMSSGFYKNUVQKH 187
 DB 123 DEKFLWMSMRLBDAMAYGRENKIDVAGFEPKLYTFSNVE--ASHHEENTNIKISK 179
 DB 188 VTFNQVKGIGFGETSDCIGKISFPATOQAPSNSPQIFDRDTIOCLPCAIDODPYF 247
 DB 180 INLNEAIKVFGDFMSNIGQVGPAAKEIAPCFSSPRIGK--GAMCLVPAAVQDPPF 236
 QY 248 RMTRDVARPIGKPKPLHSTFPALQGQTKTNSASDNNSSITLTDMQIKIV 307
 DB 237 RLARDKAKALGKPKPSIYVSLPDLKGVNRMSASDPNSIYLDQAQTIRKKIAYAY 296
 QY 308 SGGRDTIEHHOFGGNQDVDSFMVLTFFLEDDKLEQIRKQDTSQAMLTGELKALIEV 367
 DB 297 SGCRKTLEHHERBKGGIDVDPPEYKFLDQOLEKSYGSGYIKBETKEMKCKCVVV 356
 QY 368 LQPLIAEHQARKEVTDIEVKEFMPTRK 395
 DB 357 IOFPVSRVQESKRKVDDLRAFIDINK 384
 RESULT 11
 Q8U453 PRELIMINARY; PRT; 385 AA.
 ID Q8U453
 AC Q8U453;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE TRYptophanyl-TRNA synthetase.
 GN PR0241.
 OS Pyrococcus furiosus.
 OC Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OC NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE010149; AAL80365.1; -.
 KW Aminoacyl-TRNA synthetase; Complete proteome.
 SQ SEQUENCE; PR0139; 385 AA; 45178 MW; 3A7A628958200CCC CRC64;
 Query Match 39.1%; Score 826.5; DB 17; Length 385;
 Best Local Similarity 45.9%; Pred. No. 1.8e-62;
 Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;
 QY 11 BDFF-DPDPWVQTSAKGKIDYDKLVRGGSSKIDKSLINRERATCOPRHFLR 69
 DB 2 EEEFKVTPWEVGI---IDINLKQBGSPSPLDQILERARTLTKSELPIFPRRFKFFS 57
 QY 70 HRDMNQTLDAYENKPKPFLYTRGLGPSEAMHGHLIPLPFIFTRKWLQDVFNVLVI 129
 DB 58 HRDYDKVLDYEOGKGRFLYTRGLGPSSG-PMHGHTIPPFATKWLQDVFNVLVI 116
 QY 130 KWLKD-LTDOAYGDAVENAKDIAEGEDINKPFPISLDYGMSSGFYKNUVQKH 188
 DB 117 KLFKENTPFDKTYWQNYLDIAVGFDKTFIQNFONRPF---TKYEMAIIAKI 172
 QY 189 TNQVKGIGFGETSDCIGKISFPATOQAPSNSPQIFDRDTIOCLPCAIDODPYF 248
 DB 173 NFMSAKAVFGTPEQSKEGMFFPAQAPTP-----FEKK--RCLLPAIDODPYW 222

RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21937647; PubMed=11930144;
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shukhova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Steeter K.O.,
 RA Mal'kikh A.G., Koonin E.V., Kozakov S.A.; Methanopyrus kandleri AV19
 RT "the complete genome of hyperthermophile and monophyletic of archaeal methanogens";
 RT proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
 DR EMBL: AE010675; AACM03625.1; -.
 KW Aminocetyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 374 AA; 42733 MW; ODB4527931B828 CRC54;

Query Match 21.4%; Score 453; DB 17; Length 374;
 Best Local Similarity 32.2%; Pred. No. 1.7e-30; Mismatches 148; Indels 42; Gaps 12;
 Matches 124; Conservative 71; Mismatches 148; Indels 42; Gaps 12;

OY 15 VPDPWTQVQSSAKGIDYDKLIVRGSSKIDKEILINRERATGORPHRLARGFFSHDM 74
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 2 IDPFDVDE----VDYERLTTEFGIRPIDEKV----RELLPRPFPLDGRIGVFGHDYD 51

OY 75 QVDAVHENKKPFVLYTGRGPSEAMHVGHLIPPIFTKWLQDVNVPLVIQMTDEKYLW 134
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 52 SELKDYNOKKLVLVSLSGMRSR-MHGHKTVIDQLVYQEMDKVYVPLDLEAHAR 110
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 135 DLTDQAYQDVAEN-AKQDITACCPDIN---KTFIFSDLYMGMSGFYKNTVKQHVT 189
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 111 NMIDDLDRAHKIAVEBVLYNVALGLLDLDPDCEYLOSE---RKTVQRMALLAGSLT 164
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Oy 190 FNOVKGIGFTSDCIGKISFPATQAOAASFNSFSPQLRDRDIO---CLPCAINDP 245
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 165 WNTVTKNTYGFPTGETNMGHAFAPTVQADTL--HPQ----EIEGPHRVLPVPGWDPP 215
 :|||:|||:|||:|||:|||:|||:
 Oy 246 YFRMTRDYAPRIGYPKPALLHSTPPALOGAQTMKSASDPNNSIIFUTDQAKIKKHN 305
 :|||:|||:|||:|||:|||:|||:|||:|||:
 Db 216 HMLRTDIAEKLKPLKASTYHFMFTGJGG--KNSSKPNTAFLDTPEAKY-WN 272
 :|||:|||:|||:|||:|||:|||:
 Oy 193 VKCIGFTSDCIGKISFPATQAPSNSFSPQLFRDRDQCLICLCAIDDPYFWRD 252
 :|||:|||:|||:|||:|||:
 Db 167 LSAIYGSGSETSLSHMSLVAQADILQ--POLEERGGPKPVVVPVGPDODPHLRG 223
 :|||:|||:|||:
 Oy 253 VAPRIG-----YP----- 260
 :|||:
 Db 224 LAGKOMMRVEREEDVKGKVLVSRGKTAKEALOBLLKKIPKGKVKYEBHDVLEYD 283
 :|||:
 Oy 261 ----- 299
 :|||:
 Db 284 LAGLKLUREVTEFGGYAFIPPASTYHRFMGLOGG---KMSSTIPESQIALTDSPKGA 341
 :|||:
 Oy 300 TKVNKHASSGARDTIEHRHQGNCNDVSYFVLTPL-EDDKLQIRKQYTSGAMLTC 358
 :|||:
 Db 342 KRY-KRATGCGCTVLEBKKLGKPKBSVBLMLFHIASDEELBKQBCISGTRMC 400
 :|||:
 Oy 359 ELKKALIEVFLQBLIAHQARRKEVTDIVKEF 390
 :|||:
 Db 401 SKQLAKEKMQEFIKOHQEKK-ELAREHLDY 431
 :|||:
 SQ SEQUENCE 437 AA; 9067 MW; 10DF8BBBBETAJ365 CRC64;

Query Match 15.6%; Score 329.5; DB 17; Length 437;
 Best Local Similarity 25.0%; Pred. No. 8.1e-20; Mismatches 171; Indels 101; Gaps 14;
 Matches 113; Conservative 67; Mismatches 171; Indels 101; Gaps 14;

OY 15 VPDPWTQVQSSAKGIDYDKLIVRGSSKIDKEILINRERATGORPHRLARGFFSHDM 74
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 55 QFAEAEMTGAPPSVMDGFMPSGK-VHLGHKMMMDQIVWHQEM-GASAFIGIADREARSVR 112

OY 135 DLTDQAYQDVAEN-AKQDITACCPDIN---KTFIFSDLYMGMSGFYKNTVKQHVT 189
 :|||:|||:|||:|||:|||:|||:
 Db 113 GFSWQKCREBIVGEVYILSIALGPKD----GLYFOSGCCSVKDALAFELGAKVNFSE 166
 :|||:|||:
 Oy 193 VKCIGFTSDCIGKISFPATQAPSNSFSPQLFRDRDQCLICLCAIDDPYFWRD 252
 :|||:|||:|||:|||:
 Db 167 LSAIYGSGSETSLSHMSLVAQADILQ--POLEERGGPKPVVVPVGPDODPHLRG 223
 :|||:|||:
 Oy 253 VAPRIG-----YP----- 260
 :|||:
 Db 224 LAGKOMMRVEREEDVKGKVLVSRGKTAKEALOBLLKKIPKGKVKYEBHDVLEYD 283
 :|||:
 Oy 261 ----- 299
 :|||:
 Db 284 LAGLKLUREVTEFGGYAFIPPASTYHRFMGLOGG---KMSSTIPESQIALTDSPKGA 341
 :|||:
 Oy 300 TKVNKHASSGARDTIEHRHQGNCNDVSYFVLTPL-EDDKLQIRKQYTSGAMLTC 358
 :|||:
 Db 342 KRY-KRATGCGCTVLEBKKLGKPKBSVBLMLFHIASDEELBKQBCISGTRMC 400
 :|||:
 Oy 359 ELKKALIEVFLQBLIAHQARRKEVTDIVKEF 390
 :|||:
 Db 401 SKQLAKEKMQEFIKOHQEKK-ELAREHLDY 431
 :|||:
 SQ SEQUENCE 437 AA; 9067 MW; 10DF8BBBBETAJ365 CRC64;

RESULT 15

OBTUAL PRELIMINARY; PRT; 437 AA.

ID OBTUAL; AC OBTUAL; DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE TRYPTOPHANYL-tRNA synthetase.

GN TRPS OR MA0172.

OS Methanobarcina acetivorans.

OC Archaea; Buryarchaeota; Methanococci; Methanomicrobia; Methanomicrobiales; Methanomicrobium; Methanomicrobium acetivorans.

OX NCBI-TAXID:2214;

RN [1]

RN SPORSEQUENCE FROM N.A.

RC STRAIN=C2A / ATCC 35395 / DSM 2834;

RX MEDLINE=21939760; PubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., McDonald P.,
 RA FitzHugh W.W., Calvo S., Engels R.R., Smirnov S., Attoor D., Brown A.,
 RA Allen N., Navjor J., Stange-Thomann N., Bekelellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cain I., Graham D.E., Granaie D.A., Guss A.M.,
 RA Heiderich A., Ingram-Smith C., Kuettnar J.A., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Farry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;
 RT "The genome of Methanomicrobium acetivorans reveals extensive metabolic and physiological diversity";
 RT Genome Res. 12:1532-1542 (2002);
 DR EMBL: AE010675; AACM03625.1; -.
 KW Aminocetyl-tRNA synthetase; Complete proteome.

RN SEQUENCE 437 AA; 9067 MW; 10DF8BBBBETAJ365 CRC64;

Query Match 15.6%; Score 329.5; DB 17; Length 437;
 Best Local Similarity 25.0%; Pred. No. 8.1e-20; Mismatches 171; Indels 101; Gaps 14;
 Matches 113; Conservative 67; Mismatches 171; Indels 101; Gaps 14;

OY 15 VPDPWTQVQSSAKGIDYDKLIVRGSSKIDKEILINRERATGORPHRLARGFFSHDM 74
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 55 QFAEAEMTGAPPSVMDGFMPSGK-VHLGHKMMMDQIVWHQEM-GASAFIGIADREARSVR 112

OY 135 DLTDQAYQDVAEN-AKQDITACCPDIN---KTFIFSDLYMGMSGFYKNTVKQHVT 189
 :|||:|||:|||:|||:|||:|||:
 Db 113 GFSWQKCREBIVGEVYILSIALGPKD----GLYFOSGCCSVKDALAFELGAKVNFSE 166
 :|||:|||:
 Oy 193 VKCIGFTSDCIGKISFPATQAPSNSFSPQLFRDRDQCLICLCAIDDPYFWRD 252
 :|||:|||:|||:|||:
 Db 167 LSAIYGSGSETSLSHMSLVAQADILQ--POLEERGGPKPVVVPVGPDODPHLRG 223
 :|||:|||:
 Oy 253 VAPRIG-----YP----- 260
 :|||:
 Db 224 LAGKOMMRVEREEDVKGKVLVSRGKTAKEALOBLLKKIPKGKVKYEBHDVLEYD 283
 :|||:
 Oy 261 ----- 299
 :|||:
 Db 284 LAGLKLUREVTEFGGYAFIPPASTYHRFMGLOGG---KMSSTIPESQIALTDSPKGA 341
 :|||:
 Oy 300 TKVNKHASSGARDTIEHRHQGNCNDVSYFVLTPL-EDDKLQIRKQYTSGAMLTC 358
 :|||:
 Db 342 KRY-KRATGCGCTVLEBKKLGKPKBSVBLMLFHIASDEELBKQBCISGTRMC 400
 :|||:
 Oy 359 ELKKALIEVFLQBLIAHQARRKEVTDIVKEF 390
 :|||:
 Db 401 SKQLAKEKMQEFIKOHQEKK-ELAREHLDY 431
 :|||:
 SQ SEQUENCE 437 AA; 9067 MW; 10DF8BBBBETAJ365 CRC64;

Search completed: July 10, 2003, 12:31:41
 Job time : 28.2194 secs

GenCore version 5.1.5 Copyright (C) 1993 - 2003 CompuGen Ltd.									
OM protein - protein search, using sw model									
Run on: July 10, 2003, 12:26:29 ; Search time: 8.74909 Seconds									
(without alignments)									
Title: US-09-813-718-10_COPY_71_471									
Sequence: 1 SNKQDATEREEDFVDPWTV.....VTDLIVKERNPRLKLSFDFQ 401									
1900.998 Million cell updates/sec									
Post-processing: Minimum Match: 0%									
Maximum Match: 100%									
Database : SwissProt_40;*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score		Query Length		DB ID	Description			
1	2101		99.3		471	1 SYW HUMAN	SYW_HUMAN STANDARD;		PRT; 471 AA.
2	2028.5		95.9		475	1 SYW BOVIN	ID SYW_BOVIN		
3	1961.5		92.7		475	1 SYW_RABBIT	ID SYW_RABBIT		
4	1938.0		91.6		481	1 SYW_MOUSE	ID SYW_MOUSE		
5	1210.0		57.2		1 SYW_SCHPO	P23381 homologous to rabbit peptide chain release factor and bovine tryptophanyl-tRNA synthetase	ID SYW_SCHPO		
6	1163.0		55.0		432	1 SYW_CYEAST	P23612 oryctolagus cuniculus	ID SYW_CYEAST	
7	910.5		43.0		381	1 SYW_SULTO	P09582 schizosaccharomyces pombe	ID SYW_SULTO	
8	905.0		42.8		380	1 SYW_UFOLBUS	P09583 sulfolobus solfataricus	ID SYW_UFOLBUS	
9	803.0		37.9		305	1 SYW_PYRAB	P09584 pyrococcus abyssi	ID SYW_PYRAB	
10	796.0		37.6		386	1 SYW_PYRHO	P09585 pyrobaculum aerophilum	ID SYW_PYRHO	
11	735.0		34.7		375	1 SYW_PYRAE	P09586 archaeoglobus fulgidus	ID SYW_PYRAE	
12	534.5		25.3		380	1 SYW_HAHL1	P09587 thermoplasm	ID SYW_HAHL1	
13	405.5		19.4		370	1 SYW_METJEA	P09588 methanococcus jannaschii	ID SYW_METJEA	
14	397.5		18.8		364	1 SYW_METTH	P09589 methanobacter thermoautotrophicus	ID SYW_METTH	
15	386.0		18.2		134	1 SYW_ENCCU	P09590 encephalitozoon cuniculi	ID SYW_ENCCU	
16	370.5		17.5		420	1 SYW_ARCFU	P09591 archaeoglobus fulgidus	ID SYW_ARCFU	
17	353.0		17.5		374	1 SYW_AERPE	P09592 aeropyrum pernix	ID SYW_AERPE	
18	299.5		14.2		426	1 SYW_THEVO	P09593 thermoplasma volcanium	ID SYW_THEVO	
19	268.5		12.7		426	1 SYW_THEAC	P09594 archaeoglobus	ID SYW_THEAC	
20	192.0		9.1		323	1 SYW_ARCFU	P09595 archaeoglobus fulgidus	ID SYW_ARCFU	
21	185.5		8.8		341	1 SYW_STRPN	P09596 streptococcus pneumoniae	ID SYW_STRPN	
22	182.5		8.6		340	1 SYW_STRPY	P09597 streptococcus	ID SYW_STRPY	
23	175.0		8.3		341	1 SYW_COLO	P09598 clostridium	ID SYW_COLO	
24	174.5		8.2		341	1 SYW_LACLA	P09599 lactococcus	ID SYW_LACLA	
25	172.0		8.1		394	1 SYW_YEAST	P09600 saccharomyces cerevisiae	ID SYW_YEAST	
26	170.5		8.1		366	1 SYW_SULSO	P09601 sulfurovum	ID SYW_SULSO	
27	169.0		8.0		395	1 SYW_AQUAB	P09602 archaeoglobus	ID SYW_AQUAB	
28	166.5		7.9		346	1 SYW_CHLTR	P09603 chlamydial	ID SYW_CHLTR	
29	163.7		7.7		353	1 SYW_BORBU	P09604 borrelia burgdorferi	ID SYW_BORBU	
30	159.5		7.5		337	1 SYW_TREPA	P09605 treponema pallidum	ID SYW_TREPA	
31	158.0		7.5		346	1 SYW_CHLMIA	P09606 chlamydia trachomatis	ID SYW_CHLMIA	
32	152.0		7.2		344	1 SYW_CHLPN	P09607 chlamydia pneumoniae	ID SYW_CHLPN	
33	146.0		6.9		326	1 SYW_HELPC	P09608 helicobacter	ID SYW_HELPC	

RA Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kissilev L.L.;
 RT "The human gene encoding tryptophanyl-tRNA synthetase: interferon-
 RT response elements and exon-intron organization.";
 RL Gene 128:237-245(1993).
 RN [7]
 RP SEQUENCE OF 265-276; 278-295; 299-317 AND 350-365.
 RC TISSUE-Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Reamseuen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 protein database of normal human epidermal keratinocytes";
 RL Electrophoresis 13:960-969(1992).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=9225128; PubMed=1373391;
 RA Bang F.-C., Flon T., Buwitt U., Boettger E.C.;
 RT "An interferon-induced protein with release factor activity is a
 tryptophanyl-tRNA synthetase.";
 RL FEBS Lett. 300:162-166(1992).
 CC -I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I- SUBUNIT: HOMODIMER.
 CC -I- INDUCTION: BY INTERFERON GAMMA.
 CC -I- SIMILARITY: BELONGS TO CLASS-I AMINACYL-TRNA SYNTHETASE FAMILY.
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 CC

DR EMBL: M77804; AAA67324; 1; -
 DR EMBL: X59892; CAA42545; 1; -
 DR EMBL: M61715; AAAG61298; 1; -
 DR EMBL: X62570; CAA44450; 1; -
 DR EMBL: S8205; AAB3981; 1; -
 DR EMBL: X67920; CAB94198; 1; -
 DR EMBL: X67921; CAB94198; 1; JOINED.
 DR EMBL: X67922; CAB94198; 1; JOINED.
 DR EMBL: X67923; CAB94199; 1; JOINED.
 DR EMBL: X67925; CAB94199; 1; JOINED.
 DR EMBL: X67926; CAB94199; 1; JOINED.
 DR EMBL: X67927; CAB94199; 1; JOINED.
 DR PIR: A41706; A41706.
 DR PIR: A41633; A41633.
 DR PIR: JH0533; JH0533.
 DR PIR: S19246; S19246.
 DR Aarhus/Ghent-2DPAGE; 3524; IEF.
 DR PHCT-2DPAGE; P23381; -
 DR Genew; HGNC:12729; WARS.
 DR MM: 191050; -
 DR InterPro; IPR002306; TRP tRNA-synt_1b.
 DR InterPro; IPR00738; WHEP-TRS.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR Pfam; PF00458; WHEP-TRS; 1.
 DR Pfam; PF00519; tRNA-synt_1b; 1.
 DR PRINTS; PR01039; TRANASYNTHRP.
 DR TIGRFAMS; ITGR00233; TRPS; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP-TRS; 1.
 KW Aminacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 DOMAIN 19 "HIGH" REGION.
 SITE 164 173 "KNSKS" REGION.
 SITE 349 353 SY --> GD (IN REF. 3).
 DR CONFLICT 213 214 A -> R (IN REF. 4).
 FT CONFFLICT 424 424

SO SEQUENCE 471 AA; 53165 MW; E963444905A0D0 CRC64;
 QUERY Match 99.3%; Score 2101; DB 1; Length 471;
 Best Local Similarity 99.5%; Pred. No. 2.8e-165;
 Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OX 1 SNKGDATEAEEDFVDDWTVOTSSAKGIDYKLVPGSSKIDKEIJNFRATGRRPHH 60
 OX 71 SNKGDATEAEEDFVDDWTVOTSSAKGIDYKLVPGSSKIDKEIJNFRATGRRPHH 130
 DB 61 FLRGGITFSHRDNQVDAVENKKPFYLTYGRGPSSBAMHYGLHLPTFKWLDQYFNVP 120
 OX 131 FLRGRFFFSHRDNQVDAVENKKPFYLTYGRGPSSBAMHYGLHLPTFKWLDQYFNVP 190
 OX 121 LVIQMTPDEKYLWDLTQDQAVGDAVENAKDIACPFDINTPIFSDLYGMSSCPYKN 180
 DB 191 LVIQMTPDEKYLWDLTQDQAVGDAVENAKDIACPFDINTPIFSDLYGMSSCPYKN 250
 OX 181 VVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 240
 DB 251 VVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 310
 OX 241 IDDPDYFMRTRDVAPIRGYPKPAALLSTFPALQAGQTMSASDPNNSIFIQTDQKIKT 300
 DB 311 IDDPDYFMRTRDVAPIRGYPKPAALLSTFPALQAGQTMSASDPNNSIFIQTDQKIKT 370
 OX 301 KVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 401
 DB 371 KVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 430
 OX 361 KVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 471
 DB 431 KVKIQLKENTFPNQVKGIFGFTSDCIGKISFPQIAQAPSNSSPQFPRDRDQCLIPCA 471

RESULT 2

SYN_BOVIN	ID_SIW_BOVIN	STANDARD:	PRT:	475 AA.
AC P17248;	DT 01-AUG-1990 (Rel. 15, Created)	DT 01-MAY-1992 (Rel. 22, Last sequence update)	DT 15-JUN-2002 (Rel. 41, Last annotation update)	DB Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TRPS).
GN WARS.	OS Bos taurus (Bovine).	OC Bokarvota; Metacoda; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bovinae; Bos.	OX NCBI_TaxID=9913;	RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	RC TISSUE-Retina;	RC MEDLINE=9129348; PubMed=190747;	RC Garret M., Pajot B., Treteague V., Labouresse J., Merle M., Gueguen M., Sarger C., Labouresse B., Bonnet J.; Alterio J., Gendar J.-C., Benedetto J.-P., Sallafanque M.-L., Alterio J.,	
RT "A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic synthetases but near identity with mammalian peptide chain release factor.";	RT Biochemistry 30:7809-7817(1991).	RT Biochemistry 30:7809-7817(1991).	RA Garret M., Pajot B., Treteague V., Labouresse J., Merle M., Gueguen M., Sarger C., Labouresse B., Bonnet J.; Alterio J., Gendar J.-C., Benedetto J.-P., Sallafanque M.-L., Alterio J.,	
RN [2]	RN Submitted (MAR1990) to the EMBL/GenBank/DBJ databases.	RN Submitted (MAR1990) to the EMBL/GenBank/DBJ databases.	RA Labouresse J., Bonnet J.,	
RC SEQUENCE OF 17-475 FROM N.A.	RC TISSUE-Pancreas;	RC MEDLINE=9129348; PubMed=190747;	RC Submitted (MAR1990) to the EMBL/GenBank/DBJ databases.	
CC -I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +	CC diphosphate + L-tryptophanyl-tRNA(Trp).	CC SUBUNIT: HOMODIMER.	CC Submitted (MAR1990) to the EMBL/GenBank/DBJ databases.	
CC -I- SIMILARITY: BELONGS TO CLASS-I AMINACYL-TRNA SYNTHETASE FAMILY.	CC -I- SIMILARITY: BELONGS TO CLASS-I AMINACYL-TRNA SYNTHETASE FAMILY.	CC -I- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.	CC -I- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.	

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 or send an email to license@isb-sib.ch).
 CC

CC EMBL; X53918; CAA37872.1; -.
 DR InterPro; IPR002306; TIP-tRNA-synt_1b.
 DR EMBL; X52113; CAA36356.1; -.
 DR PIR; A40279; YWBO.
 DR PIR; S14540; S14540.
 DR InterPro; IPR002306; TIP-tRNA-synt_1b.
 DR InterPro; IPR000738; WHEP-TRS.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR01412; tRNA-synt_1.
 Pfam; PF00558; WHEP-TRS; 1.
 Pfam; PF00579; tRNA-synt_1b; 1.
 Prints; PRO0139; TRNAsinTHRP.
 TIGRFAMS; TIGR00233; trps; 1.
 PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 PROSITE; PS00762; WHEP-TRS; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT DOMAIN 24 69 WHEP-TRS.
 FT DOMAIN 1 117 DISPENSABLE TO THE CATALYTIC ACTIVITY.
 FT SITE 169 178 "HIGH" REGION.
 FT SITE 353 357 "KNSKS" REGION.
 FT CONFLICT 17 17 L -> M (IN REF. 2).
 FT SEQUENCE 475 AA; P7E531750137EB32 CRC64;

Query Match 95.9%; Score 2028.5; DB 1; Length 475;
 Best Local Similarity 95.8%; Pred. No. 2,6e-159; Indels 1; Gaps 1;
 Matches 384; Conservative 8; Mismatches 8; Index 1;

QY 1 SWIGPDATAEEDFVDPWTWQTSAGKIDYDKUJVRFGSSKIDELNIRERATGQRPH 60
 Db 76 SGBGLDATEADEDFVDPWTWQTSAGKIDYDKUJVRFGSSKIDELNIRERATGQRPH 135
 QY 61 PLRRGGIFFSHRDMMQVLDAVENKKPFYLTRGRGPSEAMVGHILPPFTKWLQDVENVLP 120
 Db 136 PLRRGGIFFSHRDMMQVLDAVENKKPFYLTRGRGPSEAMVGHILPPFTKWLQDVENVLP 195
 QY 121 LVQMTDDEKYLWKLTDIQLDAVDAVENAKDITACGFDPINKTIFSDIDYGMGSFYKN 180
 Db 196 LVIQMTDDEKYLWKLTDIQLDAVDAVENAKDITACGFDPINKTIFSDIDYGMGSFYKN 254
 QY 181 VVKIQKHTFNQVKIGFGETSDCIGKISFPATQAPSFSNSPQIFDRDTQCLIFCA 240
 Db 255 VVKIQKHTFNQVKIGFGETSDCIGKISFPATQAPSFSNSPQIFDRDTQCLIFCA 314
 QY 241 IDQDPYFRMTRDVAPRIGKPKALHSTFPALQOGAQTMASDPNNSSIFTDQTAQKTT 300
 Db 315 IDQDPYFRMTRDVAPRIGKPKALHSTFPALQOGAQTMASDPNNSSIFTDQTAQKTT 374
 QY 301 KUNKHAASGGGRDTEERQFGKMDVDPSFLMFTFLEDDDKLQRKDYSQSAMLCRL 360
 Db 375 KUNKHTSGGRDTEERQFGKMDVDPSFLMFTFLEDDDKLQRKDYSQSAMLCRL 434
 QY 361 KKGALIEVQPLIAHQARRKEVTDIVKFMTKRLSDFQ 401
 Db 435 KKGALIEVQPLIAHQARRKEVTDIVKFMTKRLSDFQ 475
 QY RESULT 3
 Db SYW_RABBIT STANDARD PRT; 475 AA.
 QY SYW_RABBIT STANDARD PRT; 475 AA.

QY 2 NHG_PDATAEEDFVDPWTWQTSAGKIDYDKUJVRFGSSKIDELNIRERATGQRPH 60
 Db 75 SHGPEAVDKEDFVDPWTWQTSAGKIDYDKUJVRFGSSKIDELNIRERATGQRPH 134
 QY 61 PLRRGGIFFSHRDMMQVLDAVENKKPFYLTRGRGPSEAMVGHILPPFTKWLQDVENVLP 120
 Db 135 PLRRGGIFFSHRDMMQVLDAVENKKPFYLTRGRGPSEAMVGHILPPFTKWLQDVENVLP 194
 QY 121 LVQMTDDEKYLWKLTDIQLDAVDAVENAKDITACGFDPINKTIFSDIDYGMGSFYKN 180
 Db 195 LVQMTDDEKYLWKLTDIQLDAVDAVENAKDITACGFDPINKTIFSDIDYGMGSFYKN 254
 DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (tryptophan-tRNA ligase)
 DE (Tryptophanyl-tRNA synthetase)

	FT	SITE	353	357	"RMSKS" REGION.
	FT	VARSPLIC	476	481	MISSING (IN ISOFORM 2).
	SEQUENCE		481 AA;	54282 MW;	B05A452C08074F52 CRC64;
Query Match Similarity	90.8%	Pred.	91.6%	Score	1938; DB 1; Length 481;
Best Local Matches	363;	Conservative	21;	Mismatches	16;
Indels	0;	Gaps	0;		
QY	2	NHGDATAEEDFDPTVQTSSAKGIDYDPLIVRGSKIDKELINRERATGORPHF	61		
DB	76	NCDSDATKASEDFDPTVPTTSSAKGIDYDPLIVQPGSKIDKELINRERATGORPHF	135		
QY	62	LRRGIFSSHRDNQVDAKENKPPFLYTGCGPSSAMHVLIPITPKLQLDVNVPL	121		
DB	136	LRRGIFSSHRDNQVDAKENKPPFLYTGCGPSSAMHVLIPITPKLQLDVNVPL	195		
QY	122	VIQMTDDDEKYLWMDLTQAYGDAVENAKDIAAGFDINKNPFISDLYGMMSGFYKV	181		
DB	196	VIQMSDDDEKYLWMDLTQAYGDAVENAKDIAAGFDINKNPFISDLYGMMSGFYKV	255		
QY	182	VKIQKHTFNGQKIGFTGFTSDICIGKISPAQAFSNSPQLFRDRDIOLCPAI	241		
DB	256	VKIQKHTFNGQKIGFTGFTSDICIGKISPAQAFSNSPQLFRDRDIOLCPAI	315		
QY	242	DODPYFMRDVAPRIGPKALLHSTFPALQAGTQMSADPNSSIFLTDAOKTK	301		
DB	316	DODPYFMRDVAPRIGPKALLHSTFPALQAGTQMSADPNSSIFLTDAOKISK	375		
QY	302	VKHFASGRDTIEHQRGGNCDVDFVSMWLTFFLEDKLEQIRKDYTSGAMLIGELK	361		
DB	376	VKHFASGRDTIEHQRGGNCDVDFVSMWLTFFLEDKLEQIRKDYTSGAMLIGELK	435		
QY	362	KALIEVQIQLAEHQARRKEVTDIETKEMPRKLSFDQ	401		
DB	436	KTLIDVQIQLAEHQARRKEVTDIETKEMPRKLSFDQ	475		
RC	STRAT=972;				
RC	MEDLINE=210848401; PubMed=11859360;				
RC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
RA	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
RA	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
RA	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
RA	Skelton J., Simmonds M., Squares S., Stevens K.,				
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
RA	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
RA	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
CC	MEDLINE=95108226; Pubmed=7332716;				
CC	RAJOT B., SARGER C., BONNET J., GARRET M.;				
CC	RT An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells.";				
RL	J. Mol. Biol. 242:59-603(1994).				
CC	-i- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diaphosphate + L-tryptophanyl-tRNA(Trp).				
CC	-i- SUBUNITS: HOMODIMER (BY SIMILARITY).				
CC	-i- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.				
CC	-i- TISSUE SPECIFICITY: The short isoform is widely expressed, the long form is found only in embryonic stem cells.				
CC	-i- SIMILARITY: BELONGS TO CLASS I AMINOACYL-tRNA SYNTHETASE FAMILY.				
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CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
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CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
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CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
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CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
CC	Woodward J., Voelcklaert G., Aert R., Robben J., Grymonpre B.,				
CC	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
CC	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilpert H.,				
CC	Borzym K., Langer I., Beck A., Lehachar H., Reinhardt R., Poil T.M.,				
CC	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
CC	SEQUENCE FROM N.A.				
CC	RC STRAT=972;				
CC	MEDLINE=210848401; PubMed=11859360;				
CC	Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
CC	Sgouros J., Peat N., Hayles J., Baker S., Busham D., Bowman S.,				
CC	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
CC	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
CC	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
CC	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
CC	Jones L., Jones M., Leather S., McDonald M., McLean J.,				
CC	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
CC	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E.,				
CC	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
CC	Skelton J., Simmonds M., Squares S., Stevens K.,				
CC	Taylor K., Taylor				

Qy 241 IDDPYFRMTRDVAAPRGYPKPALLHSTFPALOGAQTKMSASDPNSIFLDTAKOIKT 300
 Db 257 IDDPYFRVCRODAKLUYSKALLHHSRFPALOGSTKMSASDDTAIFWMDTPKQIQL 316

Qy 301 KINKHAASGGRRTEERHORGCCDVNUSPMVTFLEDDDEQKRDYSGAMITGEL 350
 Db 317 KINKYAFSGGQOSADHLREBLGNDPVDVAYQVLSFPKDDVFLKECYDKYKGELLSGEM 376

Qy 361 KKLIEVQOLPLAHEQARKEVTDIEVKEFMPRKL 396
 Db 377 KKLIEVQOLPLAHEQARKEVTDIEVKEFMPRKL 412

RESULT 7

SYW_SULTO SYW_SULSO STANDARD; PRT; 381 AA.

ID SYW_SULTO STANDARD; PRT; 381 AA.

AC 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (Trps)
 GN TRPS OR STV169.

OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 Sulfolobus.
 OX NCBI_TAXID=111955;

RP SYW_SULSO
 RN STRAIN=JCM 10545 / 7;
 RX MEDLINE=2156156; Pubmed=11572479;
 RA Kawarabayashi, Hino Y., Horikoshi H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Arikai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishimura K., Osukoh R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshihara T., Tanaka T., Kudo Y., Yamazaki J., Kuhida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Ohshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 DNA Res. 8:123-140(2001).
 RL 8.123-140(2001).
 CC -- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.

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RESULT 8

SYW_SULSO SYW_SULSO STANDARD; PRT; 380 AA.

ID SYW_SULSO STANDARD; PRT; 380 AA.

AC 097ZKO;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (Trps); PROTS OR SS00452.

OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 Sulfolobus.
 OX NCBI_TAXID=2287;

RP SYW_SULSO
 RN STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=2133226, Pubmed=11427726;
 RA She Q., Sung R.K., Confolomieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Wescher C.C.-Y., Clausing I.G., Curtis B.A.,
 RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozaera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duquet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Senken C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 CC -- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.

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Qy 70 HRDMNOYLDAYENKKPPYLYTGRGPSEAMHVGLIPFIFKWLQDVNPYPLVIONTDE 129
 Db 58 HRDLVLVKDYQDGKGFPLYTGRAPSL-GMIGHLPIFTKWLQDKFNVNLYIETDE 116

Qy 130 KVLMK-DLTQDAYGPAVENAKDIIAGFDINKTEFSIDYGMGSSEYKNUVKQKVY 188
 Db 117 KEMRNPNBYTLDQTRQWADNTIDIAVGENDPKTFIQDTEYI--RNMMPBIAKAKL 173

Qy 189 TNQVKCIGFTDSDCIGKSFSPAAQAPSNSNSPQIIFRDTQOCULICAIQDPYR 248
 Db 174 TEPEVATFGIQTSSWIGTWTWPAQIPT-----MFBR---RCLIPAGIDOPPYR 223

Qy 249 MTRDVAARRIGYPKPALLHSTFPALOGAQTKMSASDPNSIFLDTAKOIKTIVKHAFS 308
 Db 224 LORDIAEISLGTYKAQOHHSKLLPPLTGEGKNSQSPETAYLTDPKTVERKMYAFS 283

Qy 309 GCDTDBEHROFGNCDDVDFSMWLFPL-E-DDDKLEQIQRDYTSGAMLTGELKALIEV 367
 Db 284 GQOPTIBLRKYGNPDIDVSQWLYMFEPDDNKIKKIEDYRSQALLGKLQKLIK 343

Qy 368 LOPLIAEHQARKE 381
 Db 344 LNDFLERHRQKREE 357

Qy 70 HRDMNOYLDAYENKKPPYLYTGRGPSEAMHVGLIPFIFKWLQDVNPYPLVIONTDE 129
 Db 58 HRDLVLVKDYQDGKGFPLYTGRAPSL-GMIGHLPIFTKWLQDKFNVNLYIETDE 116

Qy 130 KVLMK-DLTQDAYGPAVENAKDIIAGFDINKTEFSIDYGMGSSEYKNUVKQKVY 188
 Db 117 KEMRNPNBYTLDQTRQWADNTIDIAVGENDPKTFIQDTEYI--RNMMPBIAKAKL 173

Qy 189 TNQVKCIGFTDSDCIGKSFSPAAQAPSNSNSPQIIFRDTQOCULICAIQDPYR 248
 Db 174 TEPEVATFGIQTSSWIGTWTWPAQIPT-----MFBR---RCLIPAGIDOPPYR 223

Qy 249 MTRDVAARRIGYPKPALLHSTFPALOGAQTKMSASDPNSIFLDTAKOIKTIVKHAFS 308
 Db 224 LORDIAEISLGTYKAQOHHSKLLPPLTGEGKNSQSPETAYLTDPKTVERKMYAFS 283

Qy 309 GCDTDBEHROFGNCDDVDFSMWLFPL-E-DDDKLEQIQRDYTSGAMLTGELKALIEV 367
 Db 284 GQOPTIBLRKYGNPDIDVSQWLYMFEPDDNKIKKIEDYRSQALLGKLQKLIK 343

Qy 368 LOPLIAEHQARKE 381
 Db 344 LNDFLERHRQKREE 357

KW	Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW	Complete proteome.
ST	81 "HIGH" REGION.
FT	81 "KMSGS" REGION.
SITE	253 257
SEQUENCE	380 AA; 44631 MW; CF8344CF63883680 CRC64;
QY	Query Match 42.8%; Score 905; DB 1; Length 380; Best Local Similarity 48.7%; Pred. No. 4.8e-67; Mismatches 68; Indels 24; Gaps 10; Matches 190; Conservative 68; MisMatches 101; Insertions 24; Deletions 24; RT
QY	11 EEDFDVDPWTQTSAGK-IDYDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 69
Db	3 DEFTTPWEV---KGKVYDQLVQFGTOKITBELKORIKNLAGDL-HVMLRNRRNFFS 56
QY	70 HRDMNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 129
Db	57 HRDLIDLVNLNDYEKSCKGFLYLTGRAPSL-GMHGHLIPFIFTKWLOEKFNAFLYBTTDE 115
QY	130 KLYMK-DLTLDQAKGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 188
Db	116 KYMANPEFTDQTRSWAYDILDAVGFNPDKTIFQDVEYI--RNMPITKAKL 172
QY	189 TENOQKGIRGFTDSICIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFR 248
Db	173 TSESEVATFGSLDASSNGLIFYPAQIAPI--MFEKK--RCLIPAGIDODPYWR 222
QY	249 MTRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 308
Db	223 LQRDIAESLGYYKAOIHSKELPLPTGPEGKNSSNPETAIVYLVDPKTWERKMKYAFS 282
QY	309 GGDRDTTEHRHQFGCGCDVDFSPMFYITFFLEDD-KLEQRKDYVTSGAMLTGELKKALIEV 367
Db	283 GGQFTIELLKRYKGGPEIDVPPQWLYIFFSEDDNRNIKEIIBERYSGKMLTGEKLQILDK 342
QY	368 LQPLIAEHQARRKETDETYKEFMPWPKLS 397
Db	343 LNNPFLKEHR-RRREBAKELVHVKDGKLA 371
RESULT 9	SYW_PYRB STANDARD: PRT: 385 AA.
ID	SYW_PYRB
AC	Q9BY11;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=GB5 / ORSAY; Heilig R.;
RT	"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution"; Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL	-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 10	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 11	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 12	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 13	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 14	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 15	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
Db	284 GRPLTKEQERKGGGEBPKCVUFWLBFIFEDDK--KLKERVYACKENGELTGECKYLIS 341
QY	367 VLQPLIAEHQARRKETDETYK 388
Db	342 KIQEFLKEHQKRRKQAEKOIETK 363
RESULT 16	SYW_PYRH STANDARD: PRT: 386 AA.
ID	SYW_PYRH
AC	Q59584;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, last sequence update)
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
DR	DR (TRPS).
GN	OS Pyrococcus abyssi.
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TAXID=22292;	
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=OP3;
RT	Medline=98344137; PubMed=9679194;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	Query Match 37.9%; Score 803; DB 1; Length 385; Best Local Similarity 45.3%; Pred. No. 1.2e-58; Mismatches 63; MisMatches 120; Indels 26; Gaps 9; Matches 173; Conservative 63; MisMatches 101; Insertions 26; Deletions 26; RT
QY	12 BDP-VPDPWTQTSAGKIDVDKLTVRGSSSKIDKEKLINRERATGORPHFLRGIFFS 70
Db	3 EDFKTPWEVEGV---VDYXKLI-EHFGPSPLTEBLKTAELTKSELPLFRKEFFSH 58
QY	71 RDMDNQVQDVAENKKPPFLYTGGRGSEAMAVGHLLPFITFKWLQDVNPVLQMTDDE 130
Db	59 RDYKVLQDVEGRGFLYTRGGRGSG-PMIGH1PFFATKWLQKFGVNMVYQITDDEK 117
QY	131 YLWKO-LTLDQAYGDAVENAKDIIACGFINKTFIFSDLDYMGMSGFVNWKVQKHT 189
Db	118 FLPKENLTFFDTKHWAYENTLIDIAVGFNPDKTIFQNSER---TKYEMAIPIAKTN 173
QY	190 FNQVKIGFGEFDSCIGKISPPAQAPSFSNSPFOIFRDRTDIOLCIPCAIDODPYFRM 249
Db	174 FSMAKAVFGFTEQSOKIGMFFFPAQIAPI--FEKR--RCLIPAKIDODPYWR 223
QY	250 TRDVAPRIGYPKPALKHSTFPALQAGQTMNSASPDNNSSIFLTAKOIKTKNKAHS 309
Db	224 QRFKASLGYKTKAIIHSKIVPSLTSLSGKNSASKPETAVALYLTSPEDVPEKWKVLPALTG 283
QY	310 GRDTTEBHQEGGNCVDYSFFMLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366

RL DNA Res. 5:55-76(1998).
 CC -I CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC
 CC
 CC EMBL; AP00007; BRA31046.1; ALT INIT.
 DR InterPro; IPR02206; TRP_tRNA_synt_1b.
 DR InterPro; IPR002305; tRNA-synt_1b.
 PFam; PF00579; tRNA-synt_1b; 1;
 DR PRINTS; PRO1039; TRANSYNTHPR.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.

FT SITE 253 257 "HIGH" REGION.
 FT SITE 253 259 "KMSKS" REGION.

Query Match Best Local Similarity 37.6%; Score 796; DB 1; Length 386; Matches 172; Conservative 68; Mismatches 125; Indels 26; Gaps 9; Sequence 386 AA; 45305 MW; 9B3C32F4028B2DD CRC64;

OY 11 EEDFVDPWVQVQTSAGKIDYDVKLIVRERSSKKDKEKLNRATGQRPHFRRGTFSH 70
 Db 3 EEFKVTPWVEGV---VDYDKLKHFGTSPLEDLERTEALKSELPIFRRKFFSH 58

OY 71 RDMDQVLDAYENKKPFYLITGRGSSEAMVHGLIPFKMQLDVNVPUVJQMTDEK 130
 Db 59 RDXDLKDYEERGFPLYTGRRPSG-PMHGIIHPFATKQMLQEKGCVNLQITDEK 117

OY 131 YLMKD-LTDQAGDAVENAKDIACGFDINKTIFPSDLYDMGMSGFYKNTVKIQKRV 189
 Db 118 FUKKENLTDDTRKMWAVNDIITAVGFDPKPFIQNSEF---TKIYEMAIPIAKIN 173

OY 190 FNGYKGIGFTDCIGKISPAQIAQSFSNPQIIRDRDIOCLIPCAADOPFRM 249
 Db 174 FSKMAKAVFGFTEOSKIGMIFFPATQIAPF---FERK---RCLPAALDOPPYWRL 223

OY 250 TRDVAPRGYKPKALLHTPPALQAGAQTKMSASPDNSIIFTDTAKOIKTKUNKHAFG 309
 Db 224 QDPAESLGYYKTAALHSKFPVSLTSLSGKMSASKPETAIALYLTSDPVEDKWKFLTG 283

OY 310 GRDTIEEHQRGGNCDVDSVFWMLTFPLDDDKLBQIRKDY--TSGAMLT3BLKKALIE 366
 Db .284 GRPTIKEQEGKGGPEPKCVVKMLEIFFEDK--KLXKERYACKNGELTCBCKRVLIS 341

OY 367 VQPLIAHQARKEVTEBIVKEMTPRKL 397
 Db 342 KQEFPLKSHQRKK-AEKLVKEKYTGKA 371

RESULT 11

SYN_PYRAE STANDARD; PRT; 375 AA.

ID SYW_PYRAE
 AC Q027US;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)

DE TRYPTOPHANYL-TRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TRPS).
 GN TRPS OR PAE3091.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoproteales; Thermoproteaceae; Pyrobaculum.
 OC NCBI_TaxID:13773;

RN [1] SEQUENCE FROM N.A.
 RP STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RC
 RK
 RA
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
 RR Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 CC -I CATALYTIC ACTIVITY: ATP + L-TRYPTOPHAN + tRNA(TRP) = AMP +
 CC diphosphate + L-tryptophanyl-tRNA(TRP).
 CC -I SUBCELLULAR LOCATION: Cytoplasmic.

-I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC
 CC
 CC EMBL; AE00911; HAL64664.1; --
 DR InterPro; IPR02305; tRNA-synt_1b.
 DR InterPro; IPR01412; tRNA-Synt_I.
 DR TIGRFAMS; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.

FT SITE 81 89 "HIGH" REGION.
 FT SITE 258 262 "KMSKS" REGION.

Query Match Best Local Similarity 34.7%; Score 735; DB 1; Length 375; Matches 162; Conservative 79; Mismatches 130; Indels 18; Gaps 11; Sequence 375 AA; 43178 MW; 3DBB85DA680F116 CRC64;

OY 70 HEDMNQVLDAYENKKPFYLITGRGSSEAMVHGLIPFKMQLDVNVPUVJQMTDE 129
 Db 57 HRDFDFIMKWHGEGRPWALYTRGLPGSC-PVHGMWPMWIKWFSKDFGLEWVFOITDE 115

OY 130 YLMKD-LTDQAGDAVENAKDIACGFDINKTIFPSDLYDMGMSGFYKNTVKIQKRV 188
 Db 116 KEYDPEMKLEATNWAYENAIDLVTALGFSPERHLITDKD1--KPLYPIAVRACKL 172

OY 189 TENVQKGIGFTDCIGKISPAQIAQSFSNPQIIRDRDIOCLIPCAADOPFR 248
 Db 173 TANTVKAFTGFUDSTWGLIFVPSLOPAVALPT--ELRERATPV--LIPCAIDQPYFR 228

OY 249 MTDVAPRGYKPKALLHTPPALQAGAQTKMSASPDNSIIFTDTAKOIKTKUNKHAFS 308
 Db 229 LARDIABALGYKPKPSTLISKFIMALTG-ESKMSASNPDSAIYLDEDEKTVRKV-MNAFT 286

OY 309 GRDTIEEHQRGGNCDVDSVFWMLTFPLDDDKLBQIRKDY--TSGAMLT3BLKKALIE 368
 Db 287 GGRTTABERKQYGGNPEVCVPVHYMLFDPPDASVERKIQDKSGALCGECKLKLHEKI 346

RESULT 12

SYW_HAANI STANDARD; PRT; 380 AA.

ID SYW_HAANI
 AC O9H666;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
DE (Trps)
GN TRPS OR TRPS2 OR VNG232G.
OS Halobacterium sp. (strain NRC-1)
OC Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1] -
RP SEQUENCE FROM N.A.
RX MEDLINE=20504433; PubMed=11016950;
RN NG W.V., Kengen S.P., Mhairs G.G., Bergquist B., Pan M.,
RA Shukla H.D., Iasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Walti R., Goo Y.A.,
RA Leitner B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenburger T.A., Peck R.F., Rohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Dennis C.J., Dennis P.P., Omer A.D.,
RA Ebbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome Sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
RN [1] -
RP SEQUENCE FROM N.A.
RX STRAIN=JAH-1 / DSM 2661 / ATCC 43067;
RN MEDLINE=9633799; PubMed=8689087;
RN Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Rich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock G.K., Merrick J.M., Glodek A.,
RA Scott J.L., Geigleman N.S.M., Weidman J.F., Funemann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Kleink H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
DR EMBL; AE005109; AAC20351; -
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR PF00579; tRNA-synt_1b; 1.
DR PRINTS; PRO1039; TRNSYNTHTRP.
DR TIGRAMS; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
DR KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 74 82 "HIGH" REGION.
FT SEQUENCE 380 AA; 41936 MW; 0F7B2B955386404F CRC64;
SQ Query Match 25.3%; Score 534.5; DB 1; Length 380;
Best Local Similarity 35.4%; Pred. No. 1.4e-36;
Matches 141; Conservative 76; Mismatches 140; Indels 41; Gaps 17;

QY 10 AEEDFDPPWTQTSAAKGIDYDKLIVRFGSSRKIDKELINRTERATGQRPHFLRAGIFFS 69
Db 3 ADGNNDTPYAVESDD---LDYKULLARFGAQNLTDDQRARFP----DPLVNRGLFYA 53
QY 70 HRDMNQTYDAYENKKPPFLYTRGLGRGSESEAMTVGHLLPFFKWLQDVNFVNVLVITMDDE 129
Db 54 GRDVDDFLTAGBQS---IVTGVGPGSG-PMHIGHAMVFYFARKLGDFEGAVVYVPLSDDE 108
QY 130 KYLWKQUTDQAYGDAVE-NAKDIIAGFDQNKTKTF--SDLDIM-GMSGFYKNUVKI 184
Db 109 KWFKDQTPAET-GDYLRLANRDLVLAGFDPBLTRIVDTRADVYPLATAFAGPV-- 164
QY 185 QKRVTFNQVKGJFGFTSDCIGKISAPAIQAPSFSNSFPQIFRDTIDQCLIPCAIDQ 244
Db 165 -RHATLQNVYG---EPDNVQGAFTPAVQFHLL--LPQVHG--EHESTLPIAVDQD 213
QY 245 PYFRMTRDVADEPRIGYP--KPALLHSTTFPALQAGQTMASADPNNSILFTDTAKOTKTKV 302
Db 214 PHVRVSVDAAKARYPKVGKPGALMQLPLSLAG-PGMSSS-AGVSIRLTDSPDTREKV 271
QY 303 NRHAFFSGGRDTIEERHQFGGNCDVDSFMVLYTFLEDDD-KLEQIRKDVTSGAMLTGELK 361

RESULT 13
SYW_METJA STANDARD; PRT; 370 AA.
ID SYW_METJA DT 01-NOV-1997 (Rel. 35, Created)
AC 058610; DT 01-NOV-1997 (Rel. 35, Last sequence update)
DB 332 DLAABRITERLAHKRRRAALGD-VTEALDAFRITDD 367
Db 332 DLAABRITERLAHKRRRAALGD-VTEALDAFRITDD 367

RN [1] -
RP SEQUENCE FROM N.A.
RX STRAIN=JAH-1 / DSM 2661 / ATCC 43067;
RN MEDLINE=9633799; PubMed=8689087;
RN Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Rich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock G.K., Merrick J.M., Glodek A.,
RA Scott J.L., Geigleman N.S.M., Weidman J.F., Funemann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Kleink H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RN Science 273:1058-1073 (1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
DR EMBL; U67582; AAB99425.1; -
DR TIGR; MJ415; -
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR PF00579; tRNA-synt_1b; 1.
DR PRINTS; PRO1039; TRNSYNTHTRP.
DR TIGRAMS; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE NEG.
DR KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 75 83 "HIGH" REGION.
FT SEQUENCE 370 AA; 42660 MW; B6C71107CP82B59D CRC64;
SQ Query Match 19.4%; Score 405.5; DB 1; Length 370;
Best Local Similarity 30.9%; Pred. No. 2.6e-26;
Matches 119; Conservative 72; Mismatches 153; Indels 41; Gaps 16;

QY 17 PWTQVSSAKGIDYKLVLRFGSSRKIDKELINRTERATGQRPHFLRAGIFFS 76
Db 8 PW--EPVAV--IDYKCTMBOFGVKPQVDPVLDLKE----HIFPRNVLGRDFERI 57

DR PROS1B; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
 KW Aminocyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 70 "HIGH" REGION.
 PT SITE 251 "RMSKS" REGION.
 SQ SEQUENCE 364 AA; 41301 MW; C2F34890338FF1D CRC64;

Query Match 18.8%; Score 397.5; DB 1; Length 364;
 Best Local Similarity 27.9%; Pred. No. 2.5e 25; Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14;
 FT SITE 255 "HIGH" REGION.

QV 15 VDPWWTQNSAKGIDYDKLTVRGSSKIDKLINRTERATGQRPHIFLRQGIFFSHRDVN 74
 2 IDPW---GSAK-LEYQDLIENFGVRPF-SEVLDEV---PEPSNLMRGGIFGRDYE 50

Db 75 QVDAYENKKPFLYTGRRGSSSEAMVGHILPPFTKWLQ---DVFNVVLVIQMTDECKWL 133
 225 TRDIANRAKEKFPTIPPSSTYHRTMGLGG--KMNSSKRPETAIFLTDDEKTWKKIFS-A 281

QV 307 FSGGRDTIEERHOFGG---NCDVDSFMVLTFLFDDDKLQEIRKDTSGAMLTGELJKKA 363
 282 KIGGRETEEEHKKGGVPEECVVTEFLY--HILDDKELAFIYQKORSGETCGKCKM 339

Db 51 RISAMKGEDEPAVWGMPCR-MHIGKHOIVDQLRW-YVRMGADTIFIPADMEYASR 108
 184 IOKHVTENQVKOIGFTSDCTGKLSFPQIAQAPSNSNFSPOIFRDRDQCLICPAIDQ 243

Db 157 LAGKVNFNEILRAlYFGTSMAHMAYAPIQVSDFIHPQDLEGGR--PVIVPGDQ 213

QV 244 DYFRMRDVAPRI---GYKPALHSTTFPALARQTKNSASDENSIPLTRAKIQ 299
 Db 214 DHIRLIRRDIARFRDRYGFELIPSSTYHRTMGGITG--KMNSSNPKSAIFLSDPPEAE 271

QV 300 TKVNHAFESGRDTIEERHOFGGNCNDVDSFMVLTFLF-DDDKLQEIRKDTSGAMLTC 358
 272 AXI-RNATGGERETLKBORLEGGVPEBCILYETLLYIMSGSDSRLEBEVYSCRNGTLMCG 330

Db 359 EIKKALIEVQLQPLIBHQARRKE 381
 331 ECKONTAEPIRKFEEELSVKRBK 353

Db

RESULT 14

SYN_METH STANDARD; PRT; 364 AA.

ID SYW_METH 026352; 15-JUN-1998 (Rel. 36, Created)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)

DE TRYPTOPHANYL-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
 DE (TRPS).
 GN TRPS OR MTM251.

OS Methanobacterium thermoautotrophicum.

OC Archaea; Euryarchaeota; Methanobacteria; Methanothermobacter.
 OC Methanobacteriaceae; Methanothermobacter.
 OC NCBI_TaxID=187420;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Delta H;

RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Deolughey C., Lee H.-M., Dubois J., Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keegle P., Lumm W., Pothier B., Oiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer D., Prabakar S., McDouall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Neeling J., Reeve J.N.; RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; RL J. Bacteriol. 179:7155-7155 (1997).

CC -I CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC DR PROS1B; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
 RA Peyrefaillade B., Broussoile V., Peyret P., Metenier G., Gouy M., Vivares C.P.;
 RR "Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene of mitochondrial evolutionary origin.";
 RL Mol. Biol. Evol. 15:683-689 (1998).

CC -I CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -I SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -I SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC DR EMBL; AB008112; AAC84157.1; -
 DR InterPro; IPR002306; TRP_tRNA-synt_1b.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_I.
 DR PR00579; tRNA-synt_1b_1.
 DR PRINTS; PR01039; TRANASYNTHTRP.
 DR TIGRFAMS; TIGR0233; trps; 1.

us-09-813-718-10_copy_71_471.rsp

DR EMBL; AJ012470; CAA10034; 1; -
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR01412; tRNA-synt_I.
 DR pfam; PF00579; tRNA-synt_1b; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
 KW Aminocetyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SITE 89 98 "HIGH" REGION.
 FT NOM TER 134 134
 SQ SEQUENCE 134 AA; 1574 MW; 60E2935B7E1344F CRC64;
 SBQUNCE

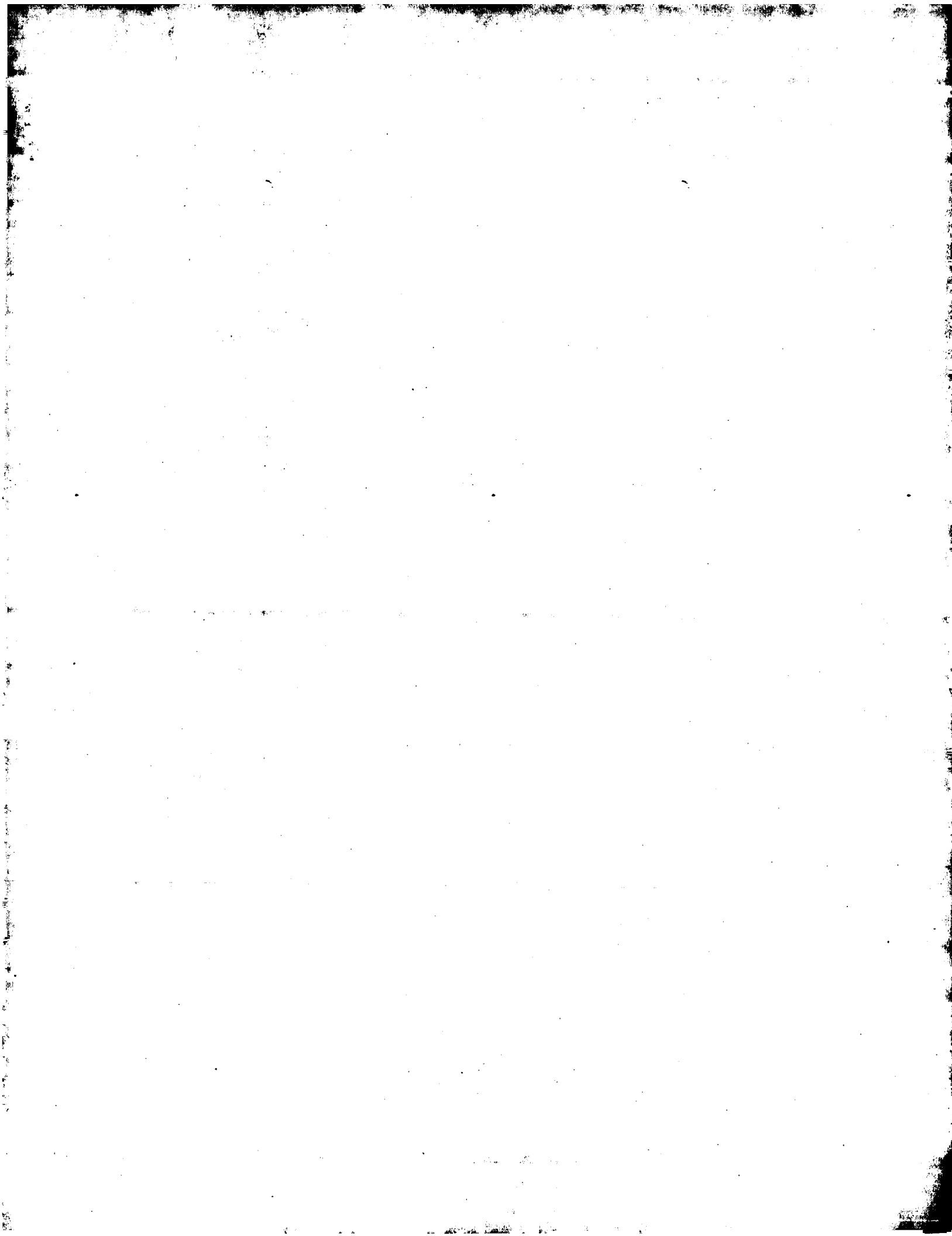
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Query Match      18.2%; Score 386; DB 1; Length 134;
Best Local Similarity 51.5%; pred No. 5. 8e-25;
Matches 68; Conservative 25; Mismatches 35; Indels 4; Gaps 1;

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Qy	12	EDFUVDPWTVOTSSAK---GIDYDULVIGRGSSKADKELINIERATGQRPHHFLRGIF	67
Db	3	EORITPMDVEVUSTDEPVVALIDKLTINOGCEKEFKNQALADRLEKLUSKGPKAHYFRRGIV	62
Qy	68	FSHRDMNOILDAYENKKPFYLTYGIGPSSEAMHVGHLIPFTKWLQDVNUPLVOMTD	127
Db	63	FAHRDFNLILDEIANRPFYLYTGAGPSKUMHIGTIPFELCKMQDAFKIRLVIQITD	122

Db Q3
128 DEKLWUJKLJD 139
123 DEKFLWKSMRLE 134



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 10, 2003, 12:28:00 ; Search time 15.5539 Seconds
(without alignments)

Sequence: 1 SNHGPDATAEAEDFVDPWTY.....VTDRIVKFEMTPRKLSDFDQ 401

Scoring table: BLOSUM62

Perfect score: 2116
Title: US-09-813-718-10_COPY_71_471

Sequence: 1 SNHGPDATAEAEDFVDPWTY.....VTDRIVKFEMTPRKLSDFDQ 401

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2101	99.3	A41706	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
2	2028.5	95.9	475	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
3	1946.5	92.0	475	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
4	1938	91.6	481	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
5	1210	57.2	395	hypothetical protein S50157
6	1163	55.0	432	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
7	907	42.9	386	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
8	803	37.9	385	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
9	626.5	29.6	301	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
10	534.9	25.3	380	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
11	409.5	19.4	370	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
12	397.5	18.8	364	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
13	386	18.2	134	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
14	370.5	17.5	420	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
15	353	16.7	374	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
16	269.5	12.7	513	tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human
17	192	9.1	323	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
18	188	8.9	364	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
19	185.5	8.8	341	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
20	185.5	8.8	341	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
21	174.5	8.2	341	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
22	172	8.1	394	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
23	170.5	8.1	366	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
24	169	8.0	395	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
25	167	7.9	351	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
26	166.5	7.9	346	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
27	164.5	7.8	895	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
28	163.5	7.7	353	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
29	7.7		460	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
30				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
31				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
32				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
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35				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
36				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
37				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
38				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
39				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
40				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
41				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
42				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
43				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
44				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human
45				tryptophanyl-tRNA synthetase (EC 6.1.1.2) [similarity] - human

ALIGNMENTS

RESULT 1				
A41706				
N	Alternate names: interferon-inducible protein IPP53; peptide-chain release factor homo1			
C	Species: Homo sapiens (man)			
C	Date: 19-May-2000 #sequence revision 19-May-2000 #text change 03-Jun-2002			
C	Accession: A11633; A41706; S19246; JN0676; JH0533; S26287			
R	Fleckner, J.; Rasmussen, H.H.; Justesen, J.			
R	Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991			
A	Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma			
A	Reference number: A11633; MUID:92107982; PMID:1763065			
A	Status: preliminary			
A	Molecule type: mRNA			
A	Cross-references: GB:X59892; NID:930820; PIDN:CAM4245.1; PIDN:g30821			
R	Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.			
J	J. Biol. Chem. 266, 24243-24248, 1991			
J	Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.			
A	Reference number: A41706; MUID:92105071; PMID:1761529			
A	Status: preliminary			
A	Molecule type: mRNA			
A	Residues: 1-471 <TLE>			
A	Cross-references: GB:W77804; NID:9184656; PIDN:AAA67324.1; PID:9184657			
R	Buettner, U.; Flohr, T.; Boettger, E.C.			
E	J. Clin. 11, 483-496, 1992			
A	Title: Molecular cloning and characterization of an interferon induced human cDNA with			
A	Reference number: S19246; MUID:92164636; PMID:1537332			
A	Status: preliminary			
A	Molecule type: mRNA			
A	Residues: 1-233, 'R', 425-471 <BUW>			
A	Cross-references: EMBL:X62570; NID:932708; PIDN:CAM4450.1; PID:932709			
A	Note: 213-Ser and 214-Tyr were also found			
R	Frolova, L.Y.; Grigorieva, A.Y.; Sudomina, M.A.; Kisseelev, L.L.			
Gene 128, 237-245, 1993				
A	Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response element			
A	Number: JN0676; MUID:33292929; PMID:7685728			
A	Accession: JN0676			
A	Molecule type: DNA			
A	Residues: 1-141; 82-471 <FRQ1>			
A	Cross-references: GB:X7918; GB:S62837; NID:937968; GB:X67919; NID:937969; GB:X67920; NID:937970; GB:X67921; NID:937971; GB:X67922; NID:937972; GB:X67923; NID:937973; GB:X67924; NID:937974; GB:X67925; GB:S62855; NID:937975; GB:X67926; NID:937976; GB:X67927; NID:937977; GB:X67928; NID:937978; GB:X67929; NID:937979; GB:X67930; NID:937980; GB:X67931; NID:937981; GB:X67932; NID:937982; GB:X67933; NID:937983; GB:X67934; NID:937984; GB:X67935; NID:937985; GB:X67936; NID:937986; GB:X67937; NID:937987; GB:X67938; NID:937988; GB:X67939; NID:937989; GB:X67940; NID:937990; GB:X67941; NID:937991; GB:X67942; NID:937992; GB:X67943; NID:937993; GB:X67944; NID:937994; GB:X67945; NID:937995; GB:X67946; NID:937996; GB:X67947; NID:937997; GB:X67948; NID:937998; GB:X67949; NID:937999; GB:X67950; NID:937990; GB:X67951; NID:937991; GB:X67952; NID:937992; GB:X67953; NID:937993; GB:X67954; NID:937994; GB:X67955; NID:937995; GB:X67956; NID:937996; GB:X67957; NID:937997; GB:X67958; NID:937998; GB:X67959; NID:937999; 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A;Cross-references: GDB:119632; OMIM:191050
 A;Map position: 14q21-14q31
 A;Introns: 33/3; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
 A;Experimental source: fibroblast
 C;Keywords: aminoacyl-tRNA synthetase; AT; ligase; protein biosynthesis
 F;19-64/Domain: amino acid-tRNA ligase repeat homology <ATL>
 Query Match 99.3%; Score 2101; DB 1; Length 471;
 Best Local Similarity 99.5%; Pred. No. 2e-163; 0; Mismatches
 Matches 399; Conservative 0; Indels 0; Gaps 0;
 Db 71 SNHGPDATTAEEAEDFDPDPTVQISSAKGIDYDKLIVRFGSSKIDKEJLNRRATGRPHH 130
 Qy 61 FLRGIGFFSHRDMDNQVDAVENENKKPFVLTGRGSPSAMHGHLLIPITFKMLQDFNVP 120
 Qy 131 FLRGGTFFSHRDMDNQVDAVENENKKPFVLTGRGSPSAMHGHLLIPITFKMLQDFNVP 190
 Db 121 LVIQMTDEEKYLKDLDQAGDAVENAKDITACGDINKFIFSDLDGMWSQFYK 180
 Db 191 LVIQMTDEEKYLKDLDQAGDAVENAKDITACGDINKFIFSDLDGMWSQFYK 250
 Qy 181 VVKLQKHVTFNQVKGIFGFTSDICGKTSFPATOQAPSFSNSFPQIFRDRDTQICLPCA 240
 Qy 241 IDDPDYFMRDVAPIRGYKPKALHSTPPFALQACTKMSASDPPSISIIFTDQAKQT 300
 Db 311 IDDPDYFMRDVAPIRGYKPKALHSTPPFALQACTKMSASDPPSISIIFTDQAKQT 370
 Db 251 VVKLQKHVTFNQVKGIFGFTSDICGKTSFPATOQAPSFSNSFPQIFRDRDTQICLPCA 310
 Qy 301 KVKNHAFSGGDRTEHRQFGGNCDVDSFWMYLTFLFEDDKLQEQRKYDYGAMTIGEL 360
 Db 371 KVKNHAFSGGDRTEHRQFGGNCDVDSFWMYLTFLFEDDKLQEQRKYDYGAMTIGEL 430
 Qy 361 KKLALIEVUQPLIAEHQARRKEVTDIYKEFMPKRSFDQ 401
 Db 431 KKLALIEVUQPLIAEHQARRKEVTDIYKEFMPKRSFDQ 471

RESULT 2

YWBO

tryptophanyl-tRNA ligase (EC 6.1.1.2) [validated] - bovine

C;Species: Bos primigenius tauris (cattle)

C;Accession: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 03-Jun-2002

R;Garret, M.; Pejot, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedett, Biochemistry 30, 7809-7817, 1991

A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic s

A;Reference number: A40279; MUID:91329348; PMID:107847

A;Accession: A40279

A;Molecule type: mRNA

A;Residues: 1-475 <GAR>

A;Cross-references: GB:W74074; EMBL:X53918; NID:9163798; PIDN:AAA307991; PID:g163799

A;Experimental source: pancreas

A;Residues: 112-124-282-287, 'N', 'B8', 'F', '289-292, 'Q', '293-294, 'I', 'R', '336-353, 423-441, 443-449

A;Experimental source: liver

A;Note: this paper is in Russian

C;Superfamily: mammalian tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homology

RESULT

A:Cross-references: GB:W74074; EMBL:X53918; NID:9163798; PID:9163799
A:Experimental source: pancreas
A:Note: part of this sequence was confirmed by protein sequencing
R.Zarganova, T.A.; Kovaleva, G.K.; Favorova, O.O.; Aevina, H.B.; Telezhinskaya, I.H.
Bioorg. Khim. 15, 1307-1311, 1989
A:Amino acid sequence of several peptides of tryptophanyl-tRNA synthetase from catfish
A:Reference number: JN0354; MUID:9211408; PMID:261684
A:Accession: JN0354
A:Molecule type: protein
A:Residues: 112-128;282-287,'N', 288, 'P', 289-292, 'Q', 293-294, 'IR';336-353,423-441,443-449
A:Experimental source: liver
A:Note: this paper is in Russian
C:Superfamily: mammalian triptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

YWRBPR
tryptop
N;Alter
C;Speci
C;Date:
C;Acces
R;Lee,
Proc. N
A;Title
A;Title

> /Domain: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
 > /Match Local Similarity 95.9%; Score 2028.5; DB 1; Length 475;
 > /Name: Match 384; Conservative 9.8%; Predicted No. 1-76-157; Indels 1; Gaps 1;
 > /Mismatches 8; Pdb 384;
 > /Sbjct: SNHGPDATEAEEDFDPWTQTSAGKIGYDKLIVRGSSKIMELNIRATGQRPH
 > /Sbjct: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 > /Sbjct: SGEGLDDEADEDFDWPWTQTSAGKIGYDKLIVRGSSKIMELNIRATGQRPH 135
 1 FLRGRGFFPSHRDMQVDAVENKPKFLYTGRRGSSEAMHVGHLIPEFTKWLQDVFNW 60
 136 FLRGICPPFSHRSRDMHQILDAYENKEPKFLYTGRRGSSEAMHVGHLIPEFTKWLQDVFNW 195
 121 LVIQWMDDEKYLWKOLTLDOAYGAVENAKDILICGFDINKTFSDIDYMGMSGFYK 180
 196 LVIQWMDDEKYLWKOLTLDOAYGAVENAKD-TTCGFDINKTFSDIDYMGMSGFYK 254
 181 WVKIQGVTRNQVKGIGFDFDSIGKISPPAQAPSNSFQIFRDTIDQCLPCA 240
 241 IDDPDPYFRMFDVAPRIGYKPKAQKLSQDPPNSIPLTDATAQIKT 300
 255 VVKIQGVTRNQVKGIGFDFDSIGKISPPAQAPSNSFQIFRDTIDQCLICA 314
 315 IDDPDPYFRMFDVAPRIGYKPKAQKLSQDPPNSIPLTDATAQIKT 374
 301 KUNKGAFSGERDTLEEHRCFGNGNDVDSFMYLTFFLEDKKLQEIRKDYTSCAMITGEL 360
 375 KVKGIAFGSGGRDTVEBHFQFGNCDDVDSFMYLTFFLEDKKLQEIRRDYTSGMLTCEL 434
 361 KKALAEVLQPLIAEQLARKEVTEBIVKEPMTPKLSDFO 401
 435 KKKELEVQPLIAEQLARKEVTEBIVKEPMTPKLSDFO 475

Best local similarity		90.8%	Pred.	No.	4	-le-150;				
Matches	363;	Conservative	21;	Mismatches	16;	Indels	0;	Gaps	0;	
QY	2	NHGDPDATEAEDFDVDPWTVQTSQSAKGIDYDKLVRFGSSKIDKLINRERATGQRPHF	60							
Db	75	SHGDPPEAVDVKEDDFDPWTVRTSSAKGIDYDKLIVQFGSSKIDKLINRERATGQRPHR	134							
QY	61	FLRIGIFFSHRDMDNQVLDAYENKKPFYLTYGRGPSEAMVGHLPFIFIKWLQDVFNTP	120							
Db	135	FLRRGIFFSHRDMDNQVLDAYENKKPFYLTYGRGPSEAMVGHLPFIFIKWLQDVFNTP	194							
QY	121	LVIQMTDDEKYLWKLDTLQDAYENKKPFYLTYGRGPSEAMVGHLPFIFIKWLQDVFNTP	180							
Db	195	LIVQMTDDEKYLWKLDTLQDAYENKKPFYLTYGRGPSEAMVGHLPFIFIKWLQDVFNTP	254							
QY	181	VVKIQKVHVTNQVKGIGFGLTSDCIGKISPAQAPSNSFQIQFHKGADQCLIPCA	240							
Db	255	VVKIQKVHVTNQVKGIGFGLTSDCIGKISPAQAPSNSFQIQFHKGADQCLIPCA	314							
QY	241	IDDPYFRMTRDVAIRGYKPALHSTFPALOQAOTQNSASPNSSPLTDPAQIKT	300							
Db	315	IDDPYFRMTRDVAIRGYKPALHSTFPALOQAOTQNSASPNSSPLTDPAQIKT	374							
QY	301	KVNKAFAFSGRDTTEFHROPGNCVDVSMLTFLEDDKLAQIRKQYTSGAMLTGEL	360							
Db	375	KVNKAFAFSGRDTTEFHROPGNCVDVSMLTFLEDDKLAQIRKQYTSGAMLTGEL	434							
QY	361	KKALIEVLQPLIAEHOQARRKEVTDIYKERTMTPRKLSFQ	401							
Db	435	KKELJDVQPLIAEHOQARRKEVTDIYKERTMTPRKLSFQ	475							
RESULT 4										
S50053	tryptophan-tRNA ligase ^f (EC 6.1.1.2) alpha-2 chain - mouse									
C.Species:	Mus musculus (house mouse)									
C.Date:	07-May-1995 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002									
C.Accession:	S50053; S50052; I49391; S31461; S3462									
R.Pajot, B.; Sarger, J.; Bonnet, J.; Garret, M.	J. Mol. Biol.	242	599-603	1994						
A.Title:	An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase									
A.Reference number:	S50052; MUID:95018226; PMID:7932716									
A.Accession:	S50053									
A.Molecule type:	mRNA									
A.Residues:	1-481 <PAJ>									
A.Cross-references:	EMBL:X63657; NID:955437; PIDN:CAA49348.1; PID:955438									
A.Genetics:	LSF									
A.Note:	introm position was determined by sequencing of genomic DNA									
A.Accession:	S50052									
A.Molecule type:	mRNA									
A.Residues:	1-475 <PAW>									
A.Cross-references:	EMBL:X63656; NID:955435; PIDN:CAA49347.1; PID:955436									
A.Genetics:	SSF									
R.Kisselov, L.L.	Biochimie	75	1027-1039	1993						
A.Title:	Mammalian tryptophanyl-tRNA synthetases									
A.Reference number:	I49391; MUID:9425729; PMID:7515282									
A.Status:	preliminary; translated from GB/EMBL/DDBJ									
A.Molecule type:	DNA									
A.Residues:	1-481 <RES>									
A.Cross-references:	EMBL:X69657; NID:955437; PIDN:CAA49348.1; PID:955438									
A.Gene:	WRS									
A.Introns:	475/2									
A.Note:	the list of introns may be incomplete; clone W13									
C.Genetics:	<SSF>									
C.Keywords:	alternative splicing; aminoacyl-tRNA synthetase; protein biosynthesis									
F1-481/ Product:	tryptophanyl-tRNA ligase alpha-2 chain long splice form #status predicted									
F1-475/ Product:	tryptophanyl-tRNA ligase alpha-2 chain short splice form #status predicted									
F1-475/ Domain:	amino acid-tRNA ligase repeat homology <ATL>									
RESULT 5										
QY	558157	hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)								
C.Species:	Schizosaccharomyces pombe									
C.Date:	13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Dec-1999									
C.Accession:	S58157; T38561									
R.Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.	submitted to the EMBL Data Library	July	1995							
A.Reference number:	S58145									
A>Status:	preliminary									
A.Molecule type:	DNA									
A.Residues:	1-395 <GEN>									
A.Cross-references:	EMBL:Z50142; NID:g1052783; PIDN:CAA90500.1; PID:91052796									
R.Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.	submitted to the EMBL Data Library	July	1995							
A.Reference number:	T38561									
A.Status:	preliminary; translated from GB/EMBL/DDBJ									
A.Molecule type:	DNA									
A.Residues:	1-395 <GE2>									
A.Experimental source:	Strain 972h; cosmid c2F7									
A.C.Genetics:	<SPAC2F7.13c									
A.Map position:	1									
C.Superfamily:	mammalian tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homolog									
Query Match	57.2%	Score	1210;	DB	2;	Length	395;			
Best Local Similarity	59.6%	Pred.	No.	7	2e-91;	Mismatches	8;	Gaps	4;	
Matches	235;	Conservative	60;			Indels				
QY	11	BEFDVDPWVQTS---SAKGIDYDKLVRFGSSKIDKLINRERATGQRPHFLRG	66							
Db	4	EQVTPDPVKGSVDGGKDYERLIVQFGSKRKPQLRERATGQRPHFLRG	63							
QY	67	FPSHRDMNQVLDAYENKKPFYLTYGRGPSEAMVGHLPFIFTKWLQDVPLVMT	126							
Db	64	FPSHRDMNQVLDAYENKKPFYLTYGRGPSSDHSFLHGMIPFWCKWLQDVPLVMT	123							

RESULT 6

tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (*Saccharomyces cerevisiae*)

C;N;Alternate names: protein HRE42; protein_0072; tryptophanyl-tRNA synthetase

C;Species: *Saccharomyces cerevisiae*

C;Accession: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 03-Jun-2002

R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

submitted to the EMBL Data Library, January 1995

Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including and a Delta.

A;Reference number: S51848

A;Accession: S51801

A;Molecule type: DNA

A;Residues: 1-432 <VAN>

A;Cross-references: EMBL:Z48149; PIDN:CAA8164.1; PIB:9663256

R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

Yeast 11, 1069-1075, 1995

A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the delta element.

A;Delta element.

A;Reference number: S51848

A;Accession: S51801

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-432 <VAN>

A;Cross-references: EMBL:Z48149; PIDN:CAA8164.1; PIB:9663256

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

R;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66791

A;Accession: S66793

A;Molecule type: DNA

A;Residues: 1-432 <DUR>

A;Cross-references: EMBL:Z74839; PIDN:CAA99110.1; PIB:91419948; GSPDB:GN00155

C;Genetics:

A;Gene: SGD:WRS1; WRS1; MIRS; YOL097c

A;Cross-references: SGD:S0005457

A;Map position: 15L

C;Superfamily: mammalian tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homology

C;Keywords: ligase

C;Experimental source: strain S28C

F;117-120/Region: ATP-binding motif (HXGH)

Query Match

Best local Similarity 55.0%; Score 1163; DB 2; Length 432; Matches 217; Conservative 71; Mismatches 10; Indels 8; Gaps 3;

Query 7 ATAAEEDFDVDPWTV----OTSSAKGIDKLVTLVRPGSSKIDKELINIERATGQPHF 61

Query 19 STVVKQEVQVTPWVEGGVDEQGRAQNIIDYKLKOFGKPVNETLKEPKQVGPHEF 78

Query 62 LRRQIGFFSHRDMQVLDAYENKPKFYLTGRGPSSSEAMHVGHLIPIFTKLUODVNVLVIQMT 121

Db 124 DDEKPLFKQGVSLEDCQRPARENADKIIAVGDFPKKTEIFMNSTYVG--GAFTQNVRIA 181

Qy 186 KHYTFNQVKGIGFTSDCIGKTSFPATOAAPSNSPQIIFRDRTDIQLPCAIDQP 245

Db 182 KCTTANQSKACGFTDSISIGKHFASTQAPASPSSSPHIFNKAQJIPCLPCAIQDP 241

Qy 246 YERMTDVAPRIGPKPALKHSTPFALQAGQTKMSASDPNNSIFLTDQAKQITKUNKH 305

Db 242 YERMTDVRSGRLKFRKPALKHHSRFPPALQGPQSKMSASRDSAIIFMTDTPNKTKNKRH 301

Qy 305 AFSGGRDTIEHHQFGNGCDVDSMFLTRFLDDDKHQIRKDYSQAMTCGKLLKALLI 365

Db 302 AFSGGATEIEHREKGGNPDVYAVQYLSFFLPDDEKKLQLYNTYKAGTLSTGEMKGBCI 361

Qy 366 EVIQPLIAHQQARKEVTDIEVKEFMT-PRKLSE 398

Db 362 KLUQQFVSDFOAARSKVBDATLUMEMDSRKLUW 395

RESULT 7

tryptophanyl-tRNA synthetase (trps) [imported] - *Sulfolobus solfataricus*

C;Species: *Sulfolobus solfataricus*

C;Accession: C90190 #sequence_revision 24-May-2001 #text_change 15-Jun-2002

R;She, O.; Singh, R. K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awazy, M. J.; Chan-Yong, I.; Jeffries, A.C.; Koera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Regan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: *Sulfolobus solfataricus* complete genome.

A;Reference number: A99139

A;Accession: C90190

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-386 <KUR>

A;Cross-references: GB:AE006641; PIDN:913813608; PIDN:ANK40778.1; GSPDB:GN00155

C;Genetics:

A;Gene: trps

Query Match Best Local Similarity 42.9%; Score 907; DB:2; Length 386; Matches 191; Conservative 68; Mismatches 110; Indels 24; Gaps 10;

Qy 8 TBAEEDFDVDPWVQTSKAG--IDYDKLIVRGSSKIDKELINIERATGQPHFURGI 66

Db 6 TMDFEFTWPWVY---KGKVYDKLIVVORGTQKTELKORIKNLGDL-HVMLRRN 59

Qy 67 FISHRDMQVLDAYENKPKFYLTGRGPSSSEAMHVGHLIPIFTKLUODVNVLVIQMT 126

Db 60 FSHRDXDVLVNDYEKSFGFLYTGAPSL-GMHIGHLIPFTKLUQEKANANUYIET 118

Qy 127 DPKSYLWK-DLTDIODOAYGDAVENAKDITACGGDINKWTFPSLDYMGWMSGFYKNTVKQ 185

Db 119 DDEKYMRAPEFEFLDQTRSWAQNLDIILAVGPNPDKFIFQDEYI--RNMVPTVKA 175

Qy 186 KHYTFNQVKGIGFTSDCIGKTSFPATOAAPSNSPQIIFRDRTDIQLPCAIDQP 245

Db 176 KULTFDDEKFLKHKLINDVNFARENKOIAIAPERDPKTPIFSQDLOQMG--GAFTYET 196

Qy 246 YERMTDVAPRIGPKPALKHSTPFALQAGQTKMSASDPNNSIFLTDQAKQITKUNKH 305

Db 226 YHRQLQDIAESIGYKQAKQINISKFLPPLTGPEGKQSSNPETAIYIVDPKVVERKIMKY 285

Db 306 AFSGGRDTIEHHQFGNGCDVDSMFLTRFLDDDKHQIRKDYSQAMTCGKLLKALLI 364

Db 286 AFSGGQFIELHRYGGNPEIDVFWQMLYFFEDDNRKIEEEVRSKGQLTGEKLQKL 345

Qy 365 IEVILQPLIAHQQARKEVTDIEVKEFMTPRKL 397

A:Experimental source: strain OR3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PHL21

Oy	185 QKRVTFENQVKGIGFTSDCIGKISFPATOAAPSFSNSFPQTFRDRTDQICLIPCAIDQ 244	Db	340 AYERVVFEFLKDLKEKRRQAKEIAVK 364
Db	165 -RHATLQNVG-----EPDNVGAOFPYPAVOTAHIL---LPOLVHG--BHETLVPIAVDOD 213		
Oy	245 PYRMRTRVAPRIGYP--KRALHSTPFPALQACQTKNSASDENSISLTDPAKQIKV 302	Db	214 PHYVRVSIDVAAKARYKVPQKPGALIMQFPLSLAG-PGKMSSS-AGVSIRLTDSPDTVREKV 271
Db	214 PHYVRVSIDVAAKARYKVPQKPGALIMQFPLSLAG-PGKMSSS-AGVSIRLTDSPDTVREKV 271		
Oy	303 NKUBAFGGDRTEBHRORGNCUDVSMYLTFLEDDD-KIEQIRKDTSGAMLTGELK 361	Db	303 NKUBAFGGDRTEBHRORGNCUDVSMYLTFLEDDD-KIEQIRKDTSGAMLTGELK 361
Db	272 RTHAYTGRASERHARKEVTBIVKFWTPRKLSFD 399		
Oy	362 KALIEVTOPLAHEQARRKEVTBIVKFWTPRKLSFD 399	Db	332 DLAADITEFLAHQRRAALGD--VTEALDAFRITDD 367
Db	332 DLAADITEFLAHQRRAALGD--VTEALDAFRITDD 367		
RESULT 11			
F64475	tryptophan-tRNA ligase (EC 6.1.1.2) - Methanococcus jannaschii	N;Alternate name: tryptophanyl-tRNA synthetase	
C;Species: Methanococcus jannaschii	C;Date: 13-Sep-1996 #sequence_change 03-Jun-2002	C;Species: Methanobacterium thermoautotrophicum	
C;Accession: F64476	C;Accession: F64476	C;Accession: E69131	
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	
S;Science 273, 1058-1073, 1996	A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii	A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis	
A;Reference number: AC4300; MUID:96337999; PMID:8688087	A;Status: preliminary; nucleic acid sequence not shown	A;Accession: E69131	
A;Accession: F64476	A;Residues: 1-364 <WTR>	A;Cross-references: GB:AE000666; NID:92621298; PIDN:AAB84757.1; PID:92621301	
A;Status: preliminary; nucleic acid sequence not shown	A;Experimental source: strain Delta H	A;Experimental source: strain Delta H	
A;Map position: FOR1375885-1376997	A;Genetics:	C;Genetics:	
A;Start codon: GRG	A;Start Codon: TTT	A;Gene: MTU251	
A;Stop codon: <BUL>	C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology	C;Superfamily: mammalian tryptophanyl-tRNA synthetase; ligase; protein biosynthesis	
C;Genetics:	Query Match 18.8%; Score 397.5;; DB 2;; Length 364;	Query Match 18.9%; Score 397.5;; DB 2;; Length 364;	
A;Map position: FOR1375885-1376997	Best Local Similarity 27.9%; Pred. No. 1.2e-24; Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14; A;Status: preliminary; nucleic acid sequence not shown	Best Local Similarity 27.9%; Pred. No. 1.2e-24; Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14;	
C;Keywords: aminoacyl-tRNA synthetase; ligase	Db	Db	
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis	Oy	Oy	
Matches 119; Conservative 72; Mismatches 153; Indels 41; Gaps 16; A;Status: preliminary; nucleic acid sequence not shown	15 VDPWTWTTSSAKGIDYDKLIVRGFSSKIDKLINRTERATGQRPHFLRGIFPSHRDMQV 76	15 VDPWTWTTSSAKGIDYDKLIVRGFSSKIDKLINRTERATGQRPHFLRGIFPSHRDMQV 76	
Oy	Db	Db	
Oy	51 RITSMKKGDFAVVGMPSGR-WHIGKOMVTDQLRW-YDRMGAETFPTADMEAVSAR 108	51 RITSMKKGDFAVVGMPSGR-WHIGKOMVTDQLRW-YDRMGAETFPTADMEAVSAR 108	
Db	2 IDPW---GSAK-LEIYDLDIENFGVGRPP-SEVLDEV---PEPSNLMRGGIIFGRDYE 50	2 IDPW---GSAK-LEIYDLDIENFGVGRPP-SEVLDEV---PEPSNLMRGGIIFGRDYE 50	
Oy	Db	Db	
Oy	135 DLTDQIYGDAVEN-AKDIACQGPDKIN-----TFFSDUDYMGMSGFYKVVK 183	135 DLTDQIYGDAVEN-AKDIACQGPDKIN-----TFFSDUDYMGMSGFYKVVK 183	
Db	109 GYDFEDSRRIALEEYIAGGYIALGLDLEKDKNLHWYILOSENLWEDVLYK 156	109 GYDFEDSRRIALEEYIAGGYIALGLDLEKDKNLHWYILOSENLWEDVLYK 156	
Oy	Db	Db	
Oy	184 IOKRVTFENQVKGIGFTSDCIGKISFPATOAAPSFSNSFPQTFRDRTDQICLIPCAIDQ 243	184 IOKRVTFENQVKGIGFTSDCIGKISFPATOAAPSFSNSFPQTFRDRTDQICLIPCAIDQ 243	
Db	Db	Db	
Oy	157 LACKVNNEFLRAlYIGFGTSMSAHMAYAPIQVSDILHPQLDIBIGGR--PVIVPGPDQ 213	157 LACKVNNEFLRAlYIGFGTSMSAHMAYAPIQVSDILHPQLDIBIGGR--PVIVPGPDQ 213	
Db	Db	Db	
Oy	244 DPYFRMRDVAPR----GYPKPALHSTPFPAQOQTKNSASDENSISLTDPAKQIKV 299	244 DPYFRMRDVAPR----GYPKPALHSTPFPAQOQTKNSASDENSISLTDPAKQIKV 299	
Db	214 DPYRILTRDIAARFRDRYGFILPSSTYHRFMGLTG--KMSNRPKSAFLSDTPEAE 271	214 DPYRILTRDIAARFRDRYGFILPSSTYHRFMGLTG--KMSNRPKSAFLSDTPEAE 271	
Oy	300 TKUNKHARSQGDRDTBHRQFGNCUDVSMYLTFLE-DDDKLQFQKDTGAMLTG 358	300 TKUNKHARSQGDRDTBHRQFGNCUDVSMYLTFLE-DDDKLQFQKDTGAMLTG 358	
Db	272 AKI-RNATGGSRETKEORELGGVPRBCIIYETLLYHMSGSDSRLEBBIYESCRNGTLMCG 330	272 AKI-RNATGGSRETKEORELGGVPRBCIIYETLLYHMSGSDSRLEBBIYESCRNGTLMCG 330	
Oy	359 ELKKALTEVLOPLIAHEQARRKE 381	359 ELKKALTEVLOPLIAHEQARRKE 381	
Db	331 ECKONTAEOFIRKEFEELSVKRB 353	331 ECKONTAEOFIRKEFEELSVKRB 353	
RESULT 13			
Oy	143806 tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)	N;Alternate name: tryptophanyl-tRNA synthetase	
C;Species: Encephalitozoon cuniculi	C;Species: Encephalitozoon cuniculi	C;Species: Encephalitozoon cuniculi	
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 03-Jun-2002	C;Accession: T43806	C;Accession: T43806	
Oy	225 TRDIANRAKEKFIPPSSTYHRFMGLTG--KMSNRPKSAFLSDTPEAE 281	R;Peyretailled, E.; Broussolle, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.	
Db	282 KTGGRTELEEHKKYGGVPECVVYELFLY-HLILDDKELAIYOKRSGEHLTGCKKRM 339	Mol. Biol. Evol. 15, 683-689, 1998	
Oy	364 LIEVLQPLIAHEQARRKEVTDIVK 388	A;Title: Microsporidia, mitochondrial protists, possess a 70-kDa heat shock protein gene	
A;Reference number: 222693; MUID:98277683; PMID:9615449	A;Accession: T43806	A;Accession: T43806	
A;Status: preliminary; translated from GB/EMBL/DDJB			

A;Molecule type: DNA
A;Residues: 1-134 <PRY>
A;Cross-references: EMBL:AJ102470; PIDN:CAA10034.1
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: ligase

Query Match 18.2%; Score 386; DB 2; Length 134;
Best Local Similarity 51.5%; Pred. No. 2.5e-24;
Matches 68; Conservatve 25; Mismatches 35; Indels 4; Gaps 1;

Qy 12 ERPVDPVWVQTSKAK---GIDYDKLIVRGFGSKIDKELINRERATGQRPHFLRRGIF 67
Db 3 EQRTIPDNEVVSTDEVPAVIDKINQPGCEKPNALADRIEKLUSGPKARYFERRGV 62

Qy 68 FSHRDMDQVLDAYENKPPYLITGRPSSEAMEMVGHLPFETKWLQDVNPVPLVQMTD 127
Db 63 FAHRDENLLDDEIANRPPFLYTGGRPSKTKHIGHTIPFLICKWMDAFKRLVQIQT 122

Qy 128 DEKYLWKDLTD 139
Db 123 DEKFELWKSMLRE 134

RESULT 14

B69461 tryptophanyl-tRNA synthetase (trps) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: EG9461
R;Klein, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.R.; Keichum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woose, C.R.; Ventor, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: EG9461
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule Type: DNA
A;Residues: 1-420 <KLE>
A;Cross-references: GB:AB000986; GB:AE000782; PIDN:ABA89554.1; PIDN:92689309; PIDN:ABA81476.1; PIDN:95105945; PIDN:BAAB1476.1; PIDN:95106155
A;Experimental source: strain K1
C;Genetics: ABP2461
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 16.7%; Score 353; DB 2; Length 374;
Best Local Similarity 30.4%; Pred. No. 5.2e-21;
Matches 119; Conservatve 70; Mismatches 165; Indels 38; Gaps 17;

Qy 15 VDPWTQVTSKAGIDYDKLIVRGFGSKIDKELINRERATGQRPHFLRRGIFFSRDMN 74
Db 8 LDPW---GAVEIKOYDRURTEFGRPPSETL--PLRKAGMESFLMRGIGLICHHRDD 61

Qy 75 QVLDAYENKPPYLITGRPSSEAMEMVGHLPFETKWLQDVNPVPLVQMTDDEKYLW 133
Db 62 KILEAKARGGERAVALTGFMPGSK-FHFGKLTVDOLIYLOKNGFKY--FVAIADEAAV 118

Qy 134 KDTLUQAGDAVEN-AKDIITACGFDINKT-FIESDLDNGMSGYRKYVVKIKHVTN 191
Db 119 RRIGRBEAVRLAVEEYVIANMIALGLDPKDTPYFO---TRNGTPYFRLIQLFSKVAA 174

Qy 192 QVKGFG-FPSDCIGKISFFAIQAPSFSNPQIFRDRDQICLIPCAIDQDPYFRMT 250
Db 175 EMAVLYGEIUPKAMASIT---QADILVQDLYGGYK--RVWVPGCADQDPHLRLT 227

Qy 251 RDVAPR---IGYPKDALIISTFPALQGQTKNSASDPNSISIHTDTAKOIKTKVKA 306
Db 228 RDLADMAGVVELERPASTHKLQFGLD--RNKSSSRPDTIILTDPPEVARNLKFR-A 284

Qy 307 FSGGRITIEERQEGNCND--DVSIMYLTFLEDDEKKLDIRKOTS--GAMILGEKK 362
Db 285 LTGGRATAMEBORRLLRGCVPEVSVWMDLHMPDGEVKH--YTSCRLGKILGECKQ 341

Qy 363 ALIEVQPLIAHQARRKETDEIIVEKFMPR 394
Db 342 IAWEKFLERFLAEHQSRLEKAKTIANKLVIEPR 373

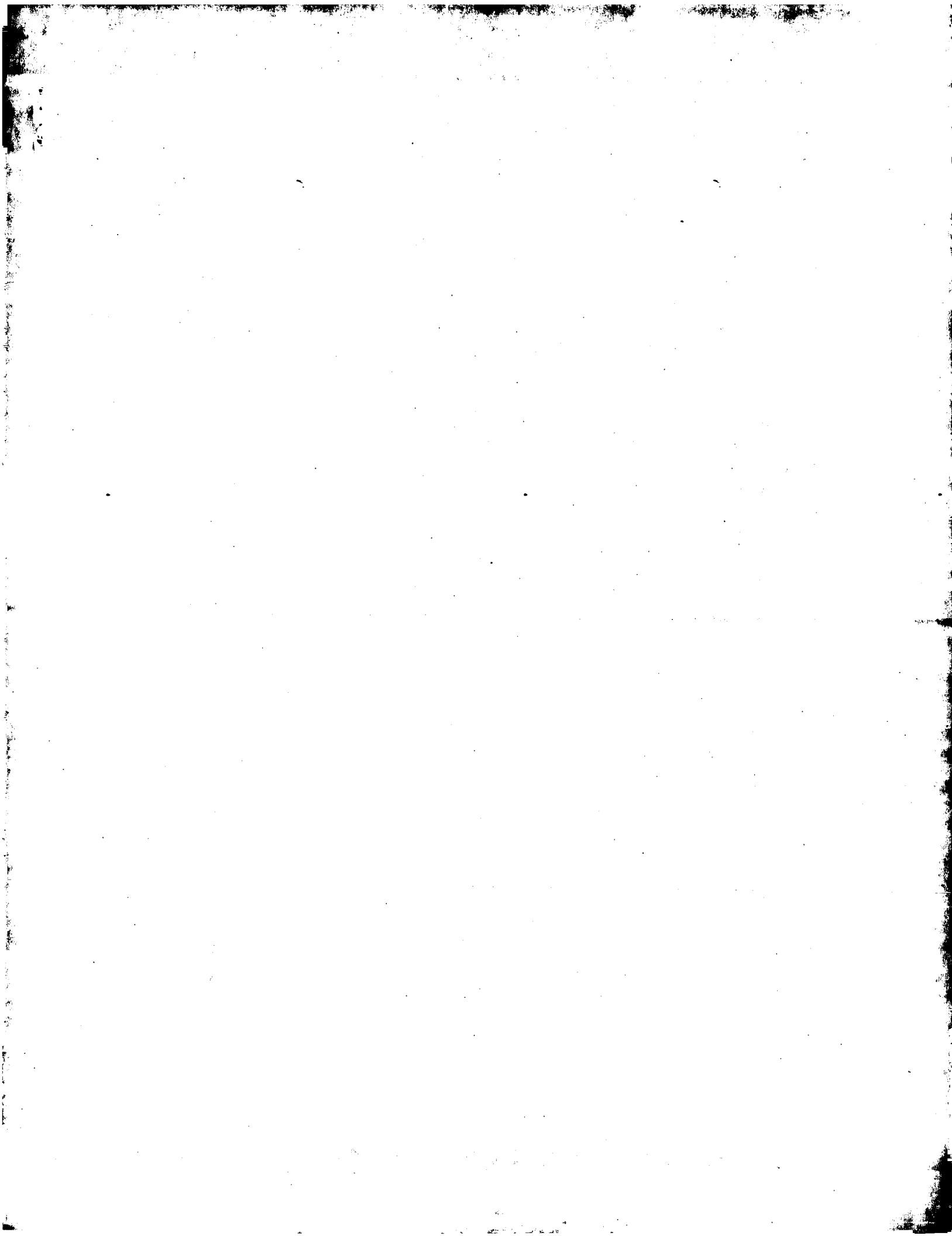
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Db 111 GLSWEKTRELGMLYIKSIIALGLREDAVIYFCG----KSSHVKCOLAFELSAEVNSEL 164

Qy 194 KGIFGFPSDCIGKISFFAIQAPSFSNPQIFRDRDQICLIPCAIDQDPYFRMTD 253
Db 165 RAYGFNSDTSIAKMFVTAOQADIL--HPLSDRCGPKPWVPGADODPHMRLLTDL 221

Qy 254 API-----
Db 222 ARARISPSFEPPEGVVRVRSRGAEVSSLRLEDFKTYHEHMDIFGEAREIERAVRKI 281
Qy 258 -----GYPKALLHSTPFPAQGQTKMSASDPNSISIHTDTAKOIKTKVKA 310
Db 282 EWEIGGFAPIPSSSTYHRFTGLTGG--KMSSSKPESYISLDPPEGAKKMK-AFTGG 338

311 RUTIEEEHRQFGNCVDVDSFMYLTFELED-DBKLEQIRKDVSQAMLTGELKKALIEVLQ 369

Search completed: July 10, 2003, 12:32:18
Job time : 16.5539 secs



Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.6	Sequence 11422, A	
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Scoring table:	BLOSUM62	Sequence 8, Appli	
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Total number of hits satisfying chosen parameters:	445758	Sequence 2, Appli	
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Maximum DB seq length:	2000000000	Sequence 52, Appli	
Post-processing:	Minimum Match 0%	Sequence 1078, A	
Database :	Maximum Match 100% Listing first 45 summaries	Sequence 59, Appli	
Published Applications AA:*		Sequence 59, Appli	
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2: /cgn2_6/prodata/2/pupcaa/PCT_NEW_PUB.pep:*		Sequence 12259, A	
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9: /cgn2_6/prodata/2/pupcaa/US09_NEW_PUB.pep:*		Sequence 59, Appli	
10: /cgn2_6/prodata/2/pupcaa/US05_PUBCOMB.pep:*		Sequence 59, Appli	
11: /cgn2_6/prodata/2/pupcaa/US10_NEW_PUB.pep:*		Sequence 59, Appli	
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14: /cgn2_6/prodata/2/pupcaa/US60_PUBCOMB.pep:*		Sequence 59, Appli	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Sequence 1306, A	
		Sequence 51, Appli	
		Sequence 51, Appli	
		Sequence 1071, A	
		Sequence 45, Appli	
		Sequence 54, Appli	
		Sequence 43, Appli	
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No.	Match Length	DB ID	Description
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2	2116	100.0	437 US-09-813-718-12
3	2116	100.0	471 US-10-126-467B2
4	2116	100.0	484 US-09-813-718-10
5	2101	99.3	471 US-09-919-0316-163
6	2101	99.3	475 US-09-925-02-558
7	1988	94.0	392 US-09-813-718-16
8	1125	53.2	433 US-10-128-714-8545
9	39.3	173	10 US-09-925-02-855
10	414.5	19.6	179 US-10-128-714-3545
11	328	15.5	85 US-09-813-718-45
12	292	13.8	85 US-09-813-718-46
13	273.5	12.9	85 US-09-813-718-48
14	263	12.4	85 US-09-813-718-47
15	226.5	10.7	142 US-09-925-320-557
16	185.5	8.8	341 10 US-09-813-242-13444
17	147	6.9	46 US-09-813-718-51
18	147	6.9	385 9 US-10-128-714-3379
19	146.5	6.9	391 9 US-10-128-714-8379
SUMMARIES			
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Sequence 14, Application US/09813718			
Publication No. US2002018266A1			
GENERAL INFORMATION:			
APPLICANT: Schimmel, Paul			
APPLICANT: Wakasugi, Keisuke			
TITLE OF INVENTION: Human Amidoacyl-tRNA Synthetase Polypeptides Useful For			
TITLE OF INVENTION: The Regulation of Angiogenesis			
FILE REFERENCE: 00-221			
CURRENT APPLICATION NUMBER: US/09/813,718			
CURRENT FILING DATE: 2001-03-21			
NUMBER OF SEQ ID NOS: 58			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO: 14			
LENGTH: 415			
TYPE: PRT			
ORGANISM: Artificial Sequence			
FEATURE:			
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: human			
US-09-813-718-14			
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Best Local Similarity	100.0%	No. 5.7e-192; Mismatches 0;	
Matches	401	Conservative 0; Indels 0; Gaps 0;	
Sequence 14, Appli			
Sequence 12, Appli			
Sequence 2, Appli			
Sequence 10, Appli			
Sequence 163, App			
Sequence 558, App			
Sequence 16, Appli			
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Qy	61 FURRGIFFSHRDMNQVYDIAVENKPKPYLYTGRGPSEAMAVGHLIPFTFWLQDVFNVP	120	
Db	62 FLRRGIFFSHRDMNQVYDIAVENKPKPYLYTGRGPSEAMAVGHLIPFTFWLQDVFNVP	121	
Qy	121 LVIQIOMTDEDKYLKDILTDAVGDAVENAKDILAGQFDNKTEPSDLQNGMSGFYKN	180	
Db	122 LVIQIOMTDEDKYLKDILTDAVGDAVENAKDILAGQFDNKTEPSDLQNGMSGFYKN	181	
Qy	181 VVKIQKRTFVNQVKGIGFTSDCIGKISPAIQAPSNSPQLFRRTDIQCLICA	240	
Db	182 VVKIQKRTFVNQVKGIGFTSDCIGKISPAIQAPSNSPQLFRRTDIQCLICA	241	

RESULT 2
US-09-813-718-12
; Sequence 12, Application US/09813718
; Publication No. US20020182666A1

GENERAL INFORMATION:
 APPLICANT: Schimmel, Paul
 APPLICANT: Wakasugi, Keisuke
 TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For Current Application Number: US/10/126,467B
 File Reference: PAU-111
 CURRENT FILING DATE: 2002-11-19
 Prior Application Number: 60/284,980
 Prior Filing Date: 2001-04-19
 Prior Application Number: 09/513,895
 Prior Filing Date: 2000-02-28
 Prior Application Number: 09/384,869
 Prior Filing Date: 1999-08-27
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.i
 SEQ ID NO: 2
 LENGTH: 471
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-126-467B-2
 ;
 Query Match 100.0%; Score 2116; DB 9; Length 471;
 Best Local Similarity 100.0%; Pred. No. 6.1e-12; Mismatches 0; Gaps 0;
 Matches 401; Conservative 0; Indels 0; Gaps 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNHGPDATAEEDPDPWTQVTSAGKIDYDYLKLIVRFGSSKIKELINRERATGQPHH 60
 Db 24 SNHGPDATAEEDPDPWTQVTSAGKIDYDYLKLIVRFGSSKIKELINRERATGQPHH 83
 Qy 61 PLRGIFFFSHRMNQVDAVENKKPFVLYTRGPSSRAMVGHLLPITFTWLDQVFNVP 120
 Db 131 PLRGIFFFSHRMNQVDAVENKKPFVLYTRGPSSRAMVGHLLPITFTWLDQVFNVP 190
 Qy 121 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 180
 Db 191 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 250
 Qy 181 VVKIQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 240
 Db 251 VVKIQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 310
 Qy 241 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 300
 Db 311 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 370
 Qy 301 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 360
 Db 371 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 430
 Qy 121 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 180
 Db 144 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 203
 Qy 181 VKLQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 240
 Db 204 VVKIQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 263
 Qy 241 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 300
 Db 264 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 323
 Qy 301 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 360
 Db 324 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 383
 Qy 361 KVLIEVQPLIAHQARKEVTDIIVEKFMTPRKLSFDQ 401
 Db 384 KVLIEVQPLIAHQARKEVTDIIVEKFMTPRKLSFDQ 424
 RESULT 3
US-10-126-467B-2
; Sequence 2, Application US/10126467B
 ;
 GENERAL INFORMATION:
 APPLICANT: Paley, Elena
 TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
 File Reference: PAU-111
 CURRENT FILING DATE: 2002-11-19
 Prior Application Number: 60/284,980
 Prior Filing Date: 2001-04-19
 Prior Application Number: 09/513,895
 Prior Filing Date: 2000-02-28
 Prior Application Number: 09/384,869
 Prior Filing Date: 1999-08-27
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.i
 SEQ ID NO: 2
 LENGTH: 471
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-126-467B-2
 ;
 Query Match 100.0%; Score 2116; DB 9; Length 471;
 Best Local Similarity 100.0%; Pred. No. 6.8e-192; Mismatches 0; Gaps 0;
 Matches 401; Conservative 0; Indels 0; Gaps 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNHGPDATAEEDPDPWTQVTSAGKIDYDYLKLIVRFGSSKIKELINRERATGQPHH 60
 Db 71 SNHGPDATAEEDPDPWTQVTSAGKIDYDYLKLIVRFGSSKIKELINRERATGQPHH 130
 Qy 61 PLRGIFFFSHRMNQVDAVENKKPFVLYTRGPSSRAMVGHLLPITFTWLDQVFNVP 120
 Db 131 PLRGIFFFSHRMNQVDAVENKKPFVLYTRGPSSRAMVGHLLPITFTWLDQVFNVP 190
 Qy 121 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 180
 Db 191 LVIQMTDDEKYLKDQTLDOQDAYDENAOKIACGFDINKTPIFSDIDYGMSSFYKN 250
 Qy 181 VVKIQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 240
 Db 251 VVKIQKHTENQVKGLGGFTSDCGIKSFPAQAPSFSNSFPQIFRRDRDIQCLPCA 310
 Qy 241 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 300
 Db 311 IDDPYPRMTRDVAPRIGYPKALLSTFPALOGAQTKMADSPPNISIFLTDQAKIQT 370
 Qy 301 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 360
 Db 371 KVNKAFASSGRTEERQFGNCVDVSFMLTFLEDDDKLEQRKYTGAMLTGEL 430
 Qy 361 KVLIEVQPLIAHQARKEVTDIIVEKFMTPRKLSFDQ 401
 Db 431 KVLIEVQPLIAHQARKEVTDIIVEKFMTPRKLSFDQ 471
 RESULT 4
US-09-813-718-10
; Sequence 10, Application US/09813718
; Publication No. US20020182666A1
;
 GENERAL INFORMATION:
 APPLICANT: Schimmel, Paul
 APPLICANT: Wakasugi, Keisuke
 TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For Current Application Number: US/09/813,718
 File Reference: 00-221
 CURRENT FILING DATE: 2001-03-21
 Prior Application Number: US/09/813,718
 Prior Filing Date: 2001-03-21
 Prior Application Number: 09/513,895
 Prior Filing Date: 2000-02-28
 Prior Application Number: 09/384,869
 Prior Filing Date: 1999-08-27
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 10
 LENGTH: 484
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: Full-length TRPS in PR20B
; US-09-813-718-10

Query Match 100.0%; Score 2116; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 7, 1e-192;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGDATEAEEBFDPWTQVTSSAKGIDYKLVIFRGSSKIDKEILNTERATGORPHH 60
Db 71 SNHGDATEAEEBFDPWTQVTSSAKGIDYKLVIFRGSSKIDKEILNTERATGORPHH 130

Qy 61 FLRRGIFFSHRMNQVDAVENKKPFYLITGRGPSSSEAMHVGHLLPFFIKWLQDVFNVP 120
Db 131 FLRRGIFFSHRMNQVDAVENKKPFYLITGRGPSSSEAMHVGHLLPFFIKWLQDVFNVP 190

Qy 121 LVIQMTDEKKYLWKLDTLDDQAYGDAVENAKDIIACGFDINKTFPSDLIYMGMSGFYKN 180
Db 191 LVIQMTDEKKYLWKLDTLDDQAYGDAVENAKDIIACGFDINKTFPSDLIYMGMSGFYKN 250

Qy 181 VVKIQKHTVNQVKGIGFFTSDCIGKISPAIQAPSNSFPOIFRRTDIOLIPCA 240
Db 251 VVKIQKHTVNQVKGIGFFTSDCIGKISPAIQAPSNSFPOIFRRTDIOLIPCA 310

Qy 241 IDQDPYFRMTRDVAPRIGYKPALLHSTFPALOCAQTMSASDPNSFLPTDQKIKT 300
Db 311 IDQDPYFRMTRDVAPRIGYKPALLHSTFPALOCAQTMSASDPNSFLPTDQKIKT 370

Qy 301 KUNKHAFFSGGRDTIEBHQFGNCDVDFSMYLTFLEDDDKLQIRKOYTSGMLTGEL 360
Db 371 KUNKHAFFSGGRDTIEBHQFGNCDVDFSMYLTFLEDDDKLQIRKOYTSGMLTGEL 430

Qy 371 KUNKHAFFSGGRDTIEBHQFGNCDVDFSMYLTFLEDDDKLQIRKOYTSGMLTGEL 430

Qy 361 KKALIEVLQLQPLIAHQARRKEVTDIVKEFMPRKLSFDFQ 401
Db 431 KKALIEVLQLQPLIAHQARRKEVTDIVKEFMPRKLSFDFQ 471

RESULT 5
US-09-919-039-163
; Sequence 163, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kager, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; CURRENT APPLICATION NUMBER: US/99/919, 039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222, 113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PBRLL Program
; SEQ ID NO: 163
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-925-302-558

Query Match 99.3%; Score 2101; DB 10; Length 475;
Best Local Similarity 99.5%; Pred. No. 1.8e-190; Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNHGDATEAEEBFDPWTQVTSSAKGIDYKLVIFRGSSKIDKEILNTERATGORPHH 60
Db 75 SNHGDATEAEEBFDPWTQVTSSAKGIDYKLVIFRGSSKIDKEILNTERATGORPHH 134

Qy 61 FLRRGIFFSHRMNQVDAVENKKPFYLITGRGPSSSEAMHVGHLLPFFIKWLQDVFNVP 120
Db 135 FLRRGIFFSHRMNQVDAVENKKPFYLITGRGPSSSEAMHVGHLLPFFIKWLQDVFNVP 194

Qy 121 LVIQMTDEKKYLWKLDTLDDQAYGDAVENAKDIIACGFDINKTFPSDLIYMGMSGFYKN 180
Db 195 LVIQMTDEKKYLWKLDTLDDQAYGDAVENAKDIIACGFDINKTFPSDLIYMGMSGFYKN 254

Qy 181 VVKIQKHTVNQVKGIGFFTSDCIGKISPAIQAPSNSFPOIFRRTDIOLIPCA 240
Db 255 VVKIQKHTVNQVKGIGFFTSDCIGKISPAIQAPSNSFPOIFRRTDIOLIPCA 314

Qy 241 IDQDPYFRMTRDVAPRIGYKPALLHSTFPALOCAQTMSASDPNSFLPTDQKIKT 300
Db 315 IDQDPYFRMTRDVAPRIGYKPALLHSTFPALOCAQTMSASDPNSFLPTDQKIKT 374

Qy 301 KUNKHAFFSGGRDTIEBHQFGNCDVDFSMYLTFLEDDDKLQIRKOYTSGMLTGEL 360
Db 375 KUNKHAFFSGGRDTIEBHQFGNCDVDFSMYLTFLEDDDKLQIRKOYTSGMLTGEL 434

Qy 361 KKALIEVLQLQPLIAHQARRKEVTDIVKEFMPRKLSFDFQ 401
Db 435 KKALIEVLQLQPLIAHQARRKEVTDIVKEFMPRKLSFDFQ 475

RESULT 7
US-09-813-718-16

Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Makasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For Current Application Number: US/09/813, 718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 392
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: human minor
US-09-813-718-16

Query Match 94%; Score 1988; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 6 9e-180; Mismatches 0; Indels 0; Gaps 0;
Matches 378; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 24 SAKGKIDYKLUVRLRGSSKIDKEJLNRTERATGORPHHLRGGIFPSHRDMNQVDAVENK 83
Db 2 SAKGKIDYKLUVRLRGSSKIDKEJLNRTERATGORPHHLRGGIFPSHRDMNQVDAVENK 61
Qy 84 KPKLYLIGGPPSSBAMHGLLPIITKWLQDFVNVLVQIMTDDEKKLWQDNLQD 143
Db 62 KPKLYLIGGPPSSBAMHGLLPIITKWLQDFVNVLVQIMTDDEKKLWQDNLQD 121
Qy 144 DAVENAKOITACGFDINKTFPSDDLYGMWSGPPYKNTVKQHVTENQVKSGPFGTSD 203
Db 122 DAVENAKOITACGFDINKTFPSDDLYGMWSGPPYKNTVKQHVTENQVKSGPFGTSD 181
Qy 204 CIGKISPAIQAPSNSFQFRDRDQICLPCALDQDPYFMRDVARYIGYKA 263
Db 182 CIGKISPAIQAPSNSFQFRDRDQICLPCALDQDPYFMRDVARYIGYKA 241
Qy 264 LHMSTFPALQGQTOKMASPDNSIIFLTDAQIKTKUNKAHSGGDTIEHROGGN 323
Db 242 LHMSTFPALQGQTOKMASPDNSIIFLTDAQIKTKUNKAHSGGDTIEHROGGN 301
Qy 324 CDDVDSFMVLTFFLEDDDKLQEIRKDYTSGAMMTGELKKALIEVLQPLIAHQARRKEV 383
Db 302 CDDVDSFMVLTFFLEDDDKLQEIRKDYTSGAMMTGELKKALIEVLQPLIAHQARRKEV 361

US-10-128-714-8545

Query Match 53.2%; Score 1125; DB 9; Length 433;
Best Local Similarity 54.7%; Pred. No. 4 2e-98; Mismatches 63; Indels 12; Gaps 5;
Matches 220; Conservative 63; MisMatches 107; Indels 12; Gaps 5;

Qy 7 ATAEAEERFVDPMY---CQSSAKGKIDYKLUVRLRGSSKIDKEJLNRTERATGORPHHL 61
Db 22 ASKAVAQVNTPEFDVSGGVDESCKLPUVDYKLVREFGATRISKELLERFERVTGRPHF 81
Qy 62 LRGIFPSHRDMNQVDAVENKPKFLYTGPPSSBAMHGLLPIITKWLQDFVNVLVQIMTDDEKKLWQDNLQD 121
Db 82 MERGIVSHRDNLNLLDQYKEQFLYTGPPSSBAMHGLLPIITKWLQDFVNVLVQIMTDDEKKLWQDNLQD 141
Qy 122 VJOMTDDBKYM-KDLTLDQYAVDANEAKOITACGFDINKTFPSDDLYGMWSGPPYKNTVKQHVTENQVKSGPFGTSD 180
Db 142 VMLTDDKYMQSQKEVDDAKKYAKANAKOITAVGFDMKKTFIFSDDPFVG-GAFYEN 199
Qy 181 VPKLKQVTTENQVKSGPFGTSDCIGKISPAIQAPSNSFQFRDPYFMRDVARYIGYKA 236
Db 200 ICMARAKITINSVRGTFEGFNDNNVGBFHFCATOSATAFATSPHPHIFTGDKKVSIIPCL 259
Qy 237 ICPAIDQDPYFMRDVARYIGYKAHSGGDTIEHROGGN 323
Db 260 ICPAIDQDPYFRCREHLSIHLAFLPRLGQKSMASVTSVAFIAFMDAPN 319
Qy 297 QIKTKUNKAHSGGDTIEHROGGNCDVDSFMVLTFFLEDDDKLQEIRKDYTSGAMMTGELKKALIEVLQPLIAHQARRKEV 356
Db 320 RIKNKINKYVAESGGQQTAELOQLGANTKDQVPQQLTFPMEDDELERIRVAYKGML 379
Qy 357 TGBLKKALIEVLQPLIAHQARRKEVDEIYKEFMPTRKLSP 398
Db 380 TGEVKQKCTIAELQAYVOFOERRAQVDEIVAEFMPRSLW 421

RESULT 8
US-10-128-714-8545

Sequence 8545, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wensi
APPLICANT: Trishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Broshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-2018-999
CURRENT APPLICATION NUMBER: US/10/128, 714

RESULT 9
US-09-925-302-855

Sequence 855, Application US/09925302
Patent No. US20044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925, 302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124, 270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 855
LENGTH: 173
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

Db 142 VIMLTDE 149

; NAME/KEY: SITE
; LOCATION: (159)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (168)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-925-302-855

Query Match 39.3%; Score 831; DB 10; Length 173;
Best Local Similarity 98.7%; Pred. No. 7. 9e-71; Mismatches 2; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 107 FIFTKWLQDVNVPLVOMTDBEKYKUWQDITDQAYGDAVENAKDITACGDDINKTPIFS 166
Db 1 FIFTKWLQDVNVPLVOMTDBEKYKUWQDITDQAYGDAVENAKDITACGDDINKTPIFS 60
Qy 167 DIDYGMGMSGFTRKVNKKIQKHTFNOYKGIRGFTSDCIGKTSPTAOAABPSFSNSPQI 226
Db 61 DIDYGMGMSGFTRKVNKKIQKHTFNOYKGIRGFTSDCIGKTSPTAOAABPSFSNSPQI 120
Qy 227 FDRRTDIOCLICAIIDDPYFMRDVAPRIGYPKRAL 264
Db 121 FDRRTDIOCLICAIIDDPYFMRDVAPRIGYPKRAL 158

RESULT 10
US-10-128-714-3545

; Sequence 3545, Application US/101288714
; Publication No. US20030119013A1

; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo

; APPLICANT: Hu, Wenqi
; APPLICANT: Zamallo, Carlos
; APPLICANT: Broshkin, Alexey M

; APPLICANT: Lemieux, Sébastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use

; FILE REFERENCE: 1018-018-999
; CURRENT APPLICATION NUMBER: US/10128, 714

; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285, 697

; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287, 066

; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295, 890

; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303, 899

; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316, 362

; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3545

; LENGTH: 179
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

US-10-128-714-3545

Query Match 15.5%; Score 328; DB 9; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.2e-23; Mismatches 0; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATEAEEDFDVPTWOTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 60
Db 24 SGEGLDATEADEDFDVPWWTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 83

Qy 61 FL 62

Db 84 FL 85

US-09-813-718-45

Query Match 13.8%; Score 292; DB 9; Length 85;
Best Local Similarity 90.3%; Pred. No. 3.2e-20; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNHGPDATEAEEDFDVPTWOTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 60
Db 24 SGEGLDATEADEDFDVPWWTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 83

Qy 61 FL 62

Db 84 FL 85

US-09-813-718-46

Query Match 13.8%; Score 292; DB 9; Length 85;
Best Local Similarity 90.3%; Pred. No. 3.2e-20; Mismatches 4; Indels 0; Gaps 0;

Matches 56; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNHGPDATEAEEDFDVPTWOTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 60
Db 24 SGEGLDATEADEDFDVPWWTSSAKGIGDYKULIVRGSSKIDKELINERATCOPRH 83

Qy 61 FL 62

Db 84 FL 85

US-09-813-718-48

RESULT 13
US-09-813-718-48
; Sequence 48, Application US/09813718
; Publication No. US201020182666A1

GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-09-813-718-48

Query Match 12.9%; Score 273.5; DB 9; Length 85;
Best Local Similarity 83.9%; Pred. No. 1.8e-18;
Matches 52; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
QY 2 NHGPD-ATPEAEDEDFDPMWVQTTSSAKGIDYDKLIVRGRSSKIDKEKLINRERATGQRPHH 60
Db 24 SHGDEADEVDDKEDFVDPMWVTRSSAKGIDYDKLIVQFGSSKIDKEKLVNIEANGQRPHR 83

QY 61 FL 62
Db 84 FL 85

RESULT 14
US-09-813-718-47
Sequence 47, Application US/09913718
Publication No. US2002018266A1
GENERAL INFORMATION:
; APPLICANT: SCHIMMEL, PAUL
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-813-718-47

Query Match 12.4%; Score 263; DB 9; Length 85;
Best Local Similarity 85.2%; Pred. No. 1.8e-17; Matches 52; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 NHGPDTEAEEDFDPMWVQTTSSAKGIDYDKLIVRGRSSKIDKEKLINRERATGQRPHH 61
Db 25 NCSDATKASEDFVDPMWVTRSSAKGIDYDKLIVQFGSSKIDKEKLINRERATGQRPHF 84

QY 62 L 62
Db 85 L 85

RESULT 15
US-09-925-302-557
Sequence 557, Application US/09925302
Patient No. US200204941A1
GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAI04
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08
PRIORITY APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 557
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (122)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (130)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (142)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-557

Query Match 10.7%; Score 226.5; DB 10; Length 142;
Best Local Similarity 70.6%; Pred. No. 1.1e-13; Matches 48; Conservative 5; Mismatches 12; Indels 3; Gaps 2;
QY 1 SNHGPDTEAEEDFDPMWVQTTSSAKGIDYDKLIVRGRSSKIDKEKLINRERATGQRPHH 60
Db 75 SNHGPDTEAEEDFDPMWVQTTSSAKGIDYDKLIVRGRSSKIDKEKLINRERATGQRPHF 133

QY 61 FLRGIF 68
Db 134 -GQGXFP 139

Search completed: July 10, 2003, 12:33:37
Job time : 21.4145 sec

QY 64 RGGFFSHRDNNQVIDAVENKKPFVLYTGRGPSSAMHVCHLIPPIFTKWLQDVENVPLVI 123
 Db 73 RGIVFFSQRDUDRDLIYERGPFPLTYGRGPSSDMHMHMFPIFTKWLQEVFDVLVI 132
 QY 124 QMTDEDEKVKW-K-DLTLDORGYDAVENAKOIIAGCDFINKTFISDLDYNGMMSGFYKVN 182
 Db 133 ELTIDDEKEFKHQHTTDDVKGPAENAKOIIAVGFPNPFNTFSQDLOMG-GAFYENV 190
 QY 183 KIQKHYTEVKQVKGFGFTDSCIGKISPAIQAOPSFNSPDIFRDRDQCLICAI 242
 Db 191 RTSRQITTTAKAVFGFTDSDCIGKIHFAQIAQTAPSSPDPDVGLGLPPKTPCILPCAI 250
 QY 243 QDPYFRMTRDVAPRIGYKPALHSTFPALQAGQTKMSASDNNSSITTDQKIKV 302
 Db 251 QDPYFRVGRDADKLRFTKPAHLAKEPALQAGASTKMSASDNNSSITTDQKIKV 310
 QY 303 NKHAFAFSGGRATIEEHRQFGCNCDVDSFVMSMLTLEDDDKLQEIRKDVTSGAMLTGELKK 362
 311 NKCAFAFSGGRATIEEHRQFGCNCDVDSFVMSMLTLEDDDKLQEIRKDVTSGAMLTGELKK 370
 QY 363 ALIEVLUQPLIAEHQARRKEVTDLEVKEFMPTRKLUF 398
 Db 371 ECITVLOQFVSAVOERRSKVDDQVKEFMPKHKLUF 406

RESULT 2
 US-08-928-100-2
 ; Sequence 2, Application US/08928100
 ; Patent No. 6046174
 ; GENERAL INFORMATION:
 ; APPLICANT: Gentry, Danile
 ; APPLICANT: Greenwood, Claire
 ; TITLE OF INVENTION: No. 6046174el trps
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASESEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 9619072..3
 ; FILING DATE: 12-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gimmi, Edward R
 ; REGISTRATION NUMBER: 38 891
 ; REFERENCE/DOCKET NUMBER: P31624-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: 610-270-4478
 ; TELEX: 610-270-5090
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 341 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-928-100-2

Query Match Score 8.8%; Score 185.5; DB 3; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;
 QY 84 KPPFLYORGPSSEAMVGHLLPPIFTKWLQDVENVPLVIQMTDEKYLWQDQAY 142
 Db 3 KPTIL-TGDRPRGK-LIIGHVYGSLR-----VLIQEEQDYMVFABLQQAL 49
 QY 143 GDAVEN-----AKDTACGFPINKUTIF--SDDYNGMSSGFYKVN--KIOK 186
 Db 50 TDHAKDQCTIVESIGNVALDYLAVGUDPKNSKTFIOSQIPELAELSMYMLUSLAR 109
 QY 187 HVTFNQYKGIFSPTDSPCIGKISPAIQA--PSFNSPDIFRDRDQCLICAI 244
 Db 110 NPVVKRISOKGFGESIFTGLVPIAQADITAFAKMY-----VPVGTDQK 156
 QY 245 PYFMRMTRD-----VAPRIGYKPALHSTFPALQAGQTKMSASDNNSSIF 290
 Db 157 PMEQOTRBIVRSFNNAYNCDVLSVERPGIYEPNE--RAGRPLGDLG-NAMOKSKS-LNNGY 212
 QY 291 LTDTAKQITKUNKHAFSGGRATIEEHRQFGCNCDVDSFVMSMLTLEDDDKLQEIRKDVTSGAMLTGELKK 348
 Db 213 LADDADTRIKKOMSMYTDPIHTRVEPKIGEN---MVFLYLDVFGRRPEDAQETADMKE 268
 QY 349 DYTSGAMLTGELKKALJELVOLPQPLIAEHQARRKEVTDI 386
 Db 269 RVQRGIGGDVVKRKYLLIEELERELGPIRERIEFAKDM 306

RESULT 3
 US-09-492-581-2
 ; Sequence 2, Application US/09492581
 ; Patent No. 634649
 ; GENERAL INFORMATION:
 ; APPLICANT: Gentry, Danile
 ; APPLICANT: Greenwood, Claire
 ; APPLICANT: Lawlor, Elizabeth
 ; TITLE OF INVENTION: No. 634609el trps
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASESEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/928,100
 ; FILING DATE: 12-SEP-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9619072..3
 ; FILING DATE: 12-SEP-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/492,581
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gimmi, Edward R
 ; REGISTRATION NUMBER: 38 891
 ; REFERENCE/DOCKET NUMBER: P31624-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: 610-270-4478
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 341 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-09-492-581-2

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-425-666-2

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Query Match 8.8%; Score 185.5; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 3.2e-12; Indels 69; Gaps 15;

Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

RESULT 4

US-09-425-666-2

; Sequence 2, Application US/09425666

; Patent No. 6416976

; GENERAL INFORMATION:

; APPLICANT: Gentry, Danile

; APPLICANT: Greenwood, Claire

; TITLE OF INVENTION: No. 6416976el trps

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEEE: SmithKline Beecham Corporation

; STREET: 709 Swedenland Road

; STATE: PA

; COUNTRY: USA

; ZIP: 19006-0399

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/425, 666

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/928, 100

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Gianni, Edward R

; REGISTRATION NUMBER: 38, 891

; REFERENCE/DOCKET NUMBER: P31624-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-4478

; TELEX: 610-270-5090

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 341 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

RESULT 5

US-08-743-130A-39

; Sequence 39, Application US/08743130A

; Patent No. 5871987

; GENERAL INFORMATION:

; APPLICANT: Sabsanfar, Mandana

; APPLICANT: Gallant, Paul L.

; APPLICANT: Shen, Xiaoyu

; APPLICANT: Tao, Nianjun

; APPLICANT: Homan, Farina

; TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02113

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743, 130A

; FILING DATE: 01-NOV-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Brook Esq., David E.

; REGISTRATION NUMBER: 22, 592

; REFERENCE/DOCKET NUMBER: CPI95-12

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 861-6240

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 409 amino acids

TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear

US-08-743-130A-39

Query Match 7.8%; Score 164.5; DB 2; Length 409;
Best Local Similarity 20.7%; Pred. No. 1e-09; Mismatches 132; Indels 107; Gaps 16;
Matches 78; Conservative 59; Mismatches 132; Indels 107; Gaps 16;

Query 76 VLDAYENK-KPFLYLTGRGPSSEAMVGHLPFI-----FTKWLQDV----F 117
27 IKDVKLEKENRKPWVKTWGPTRGK-HCQYFVPMIKAHFLKGCEVTULADHAFIDM 85
Db 118 NPLVLIOMTDDBEKLWKLDTLDOAYGDAVENAKDIIAGFDINTRTPSDLQDMGMSGF 177
86 KAPLEVVKYRAKYEFVVKAILKSINVPIERLKVVSSSYQKGDDV--MDLFKLSNIV 142

Query 178 YKVNWK---IQLHHTENQVKIGFIDSDCIGKISPAQDAPSNSNSPQIFDRD 232
143 SONDAKRAGADVTKVQANPLSLGI-----YPLMQR 351
Db 181 VDQFG-GYDQKLFVIAEENLPSIGYKRAHLMNPWGL-GOGGMSASDPNSKDI 238
233 IQCLIPCAIDQDYPRMTDVAPRIGYKPALIHSTFPALQAGQTMSASDPNSSILF 292
239 EPKVKVKVKNVSAYCAGELKONGLIAFIEVYIOPIAELKTVGEGAKFLIDRPEKYGG- 297

Query 293 DIAKQIKTKVNUHKAFSGG--ROT-----IBEROPFGN 323
239 EPKVKVKVKNVSAYCAGELKONGLIAFIEVYIOPIAELKTVGEGAKFLIDRPEKYGG- 297
324 CQUDVSMLTLEDDDKLQIRKDYTGSMGMLTGKALI---EVQLQIAHQARR 379
298 --PLSY-----DSIEQLKADFVGKLAAPPDLKSGVADKINELLAPIRAEFSS- 343

Query 380 KEVTDIEVKEFMPRK 395
Db 344 -----EEFOYAQ 351
US-08-743-130A-2

RESULT 6
; Sequence 2, Application US/08743130A
; GENERAL INFORMATION:
; APPLICANT: Sasanfar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Tao, Niannun
; APPLICANT: Tao, Jianzhili
; APPLICANT: Homan, Fariba
; TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,130A
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Eng., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPP95-12
; TELEPHONE: (617) 861-5240
; TELEX/FAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein

Query Match 7.7%; Score 162.5; DB 2; Length 409;
Best Local Similarity 20.7%; Pred. No. 1.7e-09; Mismatches 132; Indels 107; Gaps 16;
Matches 78; Conservative 59; Mismatches 132; Indels 107; Gaps 16;

Query 76 VLDAYENK-KPFLYLTGRGPSSEAMVGHLPFI-----FTKWLQDV----F 117
27 IKDVKLEKENRKPWVKTWGPTRGK-HCQYFVPMIKAHFLKGCEVTULADHAFIDM 85
Db 118 NPLVLIOMTDDBEKLWKLDTLDOAYGDAVENAKDIIAGFDINTRTPSDLQDMGMSGF 177
86 KAPLEVVKYRAKYEFVVKAILKSINVPIERLKVVSSSYQKGDDV--MDLFKLSNIV 142

Query 178 YKVNWK---IQLHHTENQVKIGFIDSDCIGKISPAQDAPSNSNSPQIFDRD 232
143 SONDAKRAGADVTKVQANPLSLGI-----YPLMQR 351
Db 181 VDQFG-GYDQKLFVIAEENLPSIGYKRAHLMNPWGL-GOGGMSASDPNSKDI 238
233 IQCLIPCAIDQDYPRMTDVAPRIGYKPALIHSTFPALQAGQTMSASDPNSSILF 292
239 EPKVKVKVKNVSAYCAGELKONGLIAFIEVYIOPIAELKTVGEGAKFLIDRPEKYGG- 297

Query 293 DIAKQIKTKVNUHKAFSGG--ROT-----IBEROPFGN 323
239 EPKVKVKVKNVSAYCAGELKONGLIAFIEVYIOPIAELKTVGEGAKFLIDRPEKYGG- 297
324 CQUDVSMLTLEDDDKLQIRKDYTGSMGMLTGKALI---EVQLQIAHQARR 379
298 --PLSY-----DSIEQLKADFVGKLAAPPDLKSGVADKINELLAPIRAEFSS- 343

Query 380 KEVTDIEVKEFMPRK 395
Db 344 -----EEFOYAQ 351
US-08-705-868-4

RESULT 7
; Sequence 4, Application US/08705868
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Discrete
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,868
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0117 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 FAX: 415-845-4116

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1184699

US-08-705-868-4

Query Match 6.3%; Score 132.5; DB 2; Length 388;
 Best Local Similarity 80%; Conservative 58%; Mismatches 121; Indels 125; Gaps 20;
 Matches 80; Predicted No. 3.6e-06;

Qy 91 GRGPPS-SEAMHVGHLIPFIFTKWLQDVFNVPVLIQWMDDE--KYLKDLTLDQ--AYGD 144
 Db 2 GDAPSPEEKHL-----LITRNLOEVIGEELKEILKERELKIYWGTTATGKPHVAYFV 54

Qy 145 AVENAKDIIAGFDINKTPFISDL-----DYMGMSSGPYKVNWKQKH--VTF 190
 Db 55 PMSKIAFLKGCEV-TILFADLHYALDNMKAPEWELLERVSYYENVIKAMLESIGVPL 112

Qy 191 NOVKGIFG-----FTSD-----CIGKISPAQAA 216
 Db 113 EKLKFPIKGTDYQVLSKEYTLDVYRLLSVVTQHDSSKGAGAEVVKQVERPLSLGQIYPLQA- 171

Qy 217 PSFSNSPQQIFRDRDIOCLICPAIDQDPYFRMTRDVAPRIGYKPALLHSTFPALOGA 276
 Db 172 -LDEEVLKV-----DAQF--GGIDQRKIFFPAEKYLPAIGSKRVHLMNPMPVPGLTG- 220

Qy 277 OTKMSASDPNNSIFLDTAKOIKTKVNHAF-----SGGRDTIEEH----- 317
 Db 221 -SKMSSEEESEKSLIDLRKEDVKKKLK-AFCPEGVNEYNGVLSPIKHLFLPLKSBFVIL 278

Qy 318 --RQFGNCNDVDSFVMLTFFLEDDDKLQEIRKDYTSGAMLTGELKKALIEVLOPLIAH 375
 Db 279 RDEKWGSGN-----KTYAVD-----LEKOPFAEVWHPGOLNSVEVALNKLU-- 321

Qy 376 QARRKEVTDETVKEFMTP--RKL 397
 Db 322 -----DPIREKFNTPALKKLA 337

RESULT 8
 US-03-123-615-4

; Sequence 4, Application US/09123615
 ; Patent No. 6593077
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Coleman, Roger
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Murry, Lynn E.
 ; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
 ; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Discrete
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/123, 615
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/705, 868

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0117 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 FAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1184699

US-09-123-615-4

Query Match 6.3%; Score 132.5; DB 3; Length 388;
 Best Local Similarity 20.8%; Predicted No. 3.6e-06; Mismatches 121; Indels 125; Gaps 20;
 Matches 80; Conservative 58; MisMatches 121; Indels 125; Gaps 20;

Qy 91 GRGPPS-SEAMHVGHLIPFIFTKWLQDVFNVPVLIQWMDDE--KYLKDLTLDQ--AYGD 144
 Db 2 GDAPSPEEKHL-----LITRNLOEVIGEELKEILKERELKIYWGTTATGKPHVAYFV 54

Qy 145 AVENAKDIIAGFDINKTPFISDL-----DYMGMSSGPYKVNWKQKH--VTF 190
 Db 55 PMSKIAFLKGCEV-TILFADLHYALDNMKAPEWELLERVSYYENVIKAMLESIGVPL 112

Qy 191 NOVKGIFG-----FTSD-----CIGKISPAQAA 216
 Db 113 EKLKFPIKGTDYQVLSKEYTLDVYRLLSVVTQHDSSKGAGAEVVKQVERPLSLGQIYPLQA- 171

Qy 217 PSFSNSPQQIFRDRDIOCLICPAIDQDPYFRMTRDVAPRIGYKPALLHSTFPALOGA 276
 Db 279 RDEKWGSGN-----KTYAVD-----LEKOPFAEVWHPGOLNSVEVALNKLU-- 321

Qy 318 --RQFGNCNDVDSFVMLTFFLEDDDKLQEIRKDYTSGAMLTGELKKALIEVLOPLIAH 375
 Db 322 -----DPIREKFNTPALKKLA 337

RESULT 9
 US-03-855-910-11

; Sequence 11, Application US/08855910
 ; Patent No. 6221640
 ; GENERAL INFORMATION:
 ; APPLICANT: Tao, Jianshi
 ; APPLICANT: Sasanar, Mandana
 ; APPLICANT: Gallant, Paul L.
 ; APPLICANT: Shen, Xiaoyu
 ; APPLICANT: Avruch, Anthony S.
 ; APPLICANT: Yu, Russell V.
 ; APPLICANT: Nair, Shamila
 ; TITLE OF INVENTION: ENTEROCOCCAL AMINOCYCL-tRNA SYNTHETASE
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
 ; NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Discrete
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/855,910
 FILING DATE: 14-MAY-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOK, David E.

REGISTRATION NUMBER: 22-592
 REFERENCE/DOCKET NUMBER: CPI95-08
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 418 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-855-910-11.

Query Match 5.4%; Score 113.5; DB 4; Length 418;
 Best Local Similarity 20.5%; Pred. No. 0.00056; Matches 82; Conservative 47; Mismatches 116; Indels 144; Gaps 19;

Matches 82; Conservative 49; Mismatches 116; Indels 144; Gaps 19;

QY 88 LYTGRRGPSSBAMVGHLLPPIFKWLQDVNVPLV----- 123
 Db 33 LYCCyDPrGDSMTHGLLPPMMRFQLAGHHPYIILGGGTGTTGDPGSGRTTVERVLQTE 92
 QY 124 -----QMTDEKYLW-KDLTLDQDAYGDAVEN-----AKOTIA 154
 Db 93 AVQHNVDLSNQMKLFLGKDAEVIMVNYYDWLBSLSLDPFLRDIYGNFVNMLAKOIVIA 152
 QY 155 CGFDINKTFIFPSIDYGMNS-GRYKNUVKIKQEVTFENOKG----- 195
 Db 153 S-RLEGISFTPEFYQIQLSIDY--TLHKKHNIOLQIGADQWGNITAGLDLIRKE 207
 QY 196 -----IRGTF----DSDCIGKISFPAlQAPSFSNSPP-QIFRRTDIOCLICAI 241
 Db 208 GPEAKVFGUTIPRMLKAQDGTKFGKTAGGAIWLPDKKTSPPFEYQFWLNDD----- 258
 QY 242 DQDPYFRMRDVAPRIGYKPKALHISTFPALQCAQTMSASDPNSSIFLTDTAQKIKT 301
 Db 259 -----RDV---IKYLK-----FPTFLDKEE-----IDALAAKEKE 286
 Qy 3.02 VNKHAfSGCRDTIEHROPGGNCVUDSVFMYLTFPLEDDKUQIRKOYTSGAMLTBLK 361
 Db 287 PGKR--EAQRRLAEE-----VTRFHDDAALERAQK--ISEALFSGNIK 326
 Qy 362 KALIEVLQ-----PLIAHQARKEVDEIKEFMPRK 395
 Db 327 DLTIEEIEOGLEHVPTV-BITKDAKNIVDWLVDEIEPSK 365

RESULT 10

US-09-352-990-28

Sequence 28, Application US/09352990

PATENT NO. 6255090

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Orozco, Buddy

APPLICANT: Rafalski, Antoni

TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase

FILE REFERENCE: BB-1191.

CURRENT APPLICATION NUMBER: US/09/352,990
 CURRENT FILING DATE: 1999-07-14
 EARLIER APPLICATION NUMBER: 60/092,866
 EARLIER FILING DATE: July 15, 1998
 NUMBER OF SEQ ID NCS: 29
 SOFTWARE: Microsoft Office 97

SEQ ID NO 28
 LENGTH: 377
 TYPE: PRT
 ORGANISM: Synechocystis sp.

US-09-352-990-28

Query Match 5.2%; Score 109; DB 4; Length 377;
 Best Local Similarity 21.0%; Pred. No. 0.0015; Matches 82; Conservative 49; Mismatches 116; Indels 144; Gaps 19;

Matches 82; Conservative 49; Mismatches 116; Indels 144; Gaps 19;

QY 68 FSHRDMMQVLDAYENKKPFYLYTGRGPSSSEAHVGHLIPLIFTKWILQDVNVPLVQMTD 127
 Db 33 FAHRSTHAM-----DKPERIL-SGVQPTGN-LHGHYLGAI-RSWEQ-----QHY 75
 QY 128 DERYLWKL-----TLDQAYGDAVENAKDITACGFDINKTIF----- 165
 Db 76 DNFFCVVLDHALAITVPHNPQTLAQ--DTLTAAALYLAGIDLQYSITFVQSHVAHSEL 132
 QY 166 -----SDDIXMGMSGFPPKVVKQKGVTNQVKIGFFDSDCTGKTSFPAIQAPS 219
 Db 133 WLJNCVTFPLNMFLQKERAVKQOENVS-----VGLLDYPVLMIA--- 174
 QY 220 SNSPPOQFRDRDIOCL---IPCA1DQDPYFRMTRDV-----APRIGPKA 263
 Db 175 -----BILYDADKVPVGQDQKQHLELTEDIVRINDKFGRDAPVLUPEPL 222
 QY 264 L-LHSTFPALQGQAQTMSASDPN--SSIFLJDTAKQIKTKONKHAFGGRTIEHRQF 320
 Db 223 IRKEGARVMSLADGTKMKSKDSESELRSRNILDPPMENIKKVK----- 266
 QY 321 GENCDVUNVSFMVLTFFLEDKOLEQTRKDYNGAMLTGELCKAL----- 364
 Db 267 ---CKTDQ-RGIWF--DDPERPECNLNTLYLTSNOTKEAVAOBCAEMGWGQFKPL 319
 QY 365 -----LEVOLPLIAHQARRKEVDEIVK 388
 Db 320 TEPAAIALEPTIQAKYAEILADRGEL-DRRIQ 349

RESULT 11

US-08-923-867-2

Sequence 2, Application US/08923867

PATENT NO. 5831809

GENERAL INFORMATION:

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION: NOVEL TRYPTOPHANYL tRNA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0319

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923,867
 FILING DATE: 04-SEP-1997
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 9619072..3
 FILING DATE: 12-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R
 REGISTRATION NUMBER: 38, 891
 REFERENCE/DOCKET NUMBER: P31624
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; MOLECULE TYPE: protein
 ; US-08-928-867-2

Query Match Similarity 5.1%; Score 108; DB 2; Length 197;
 Best Local Similarity 25.3%; Pred. No. 0.00067; Mismatches 73; Indels 24; Gaps 6;
 Matches 42; Conservative 27; MisMatches 73; Indels 24; Gaps 6;

Qy 237 IPCATDODPYRMRTRD-----VAPRIGYPKPALLHSPPALQGAOTKMSA 282
 Db 5 VPGVGTQPKPMIBQTRBIVRSFNNAVNCDVLVPEEGIYIPENE--RAGRLPGLDG-NAKMSK 61

Qy 283 SDPNSSIFLTDTAKOIKTKVVKHAFSGGRDTIEBRHQFGNCNDVSVFMYLTF--LEDD 340
 Db 62 S-LNNGIYLADDATLTKVMSMTPDHIREVPEKIEGN---MVFHYLDVGRPEDA 116

Qy 341 DKLEQTRKDVTSGAMLTGELKKALIEVQLAEHQARKEVTDI 386
 Db 117 QEIADMKERYORGGLGDVKTKYVLLERELGPIRRERRFAKM 162

RESULT 12
 US-08-928-100-4
 Sequence 4, Application US/08928100
 Patent No. 6046174

GENERAL INFORMATION:
 APPLICANT: Gentry, Danile
 APPLICANT: Greenwood, Claire
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: No. 6046174el trps
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0939.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/183, 134
 FILING DATE:
 CLASSIFICATION:
 PRIORITY INFORMATION:
 APPLICATION NUMBER: 9619072..3
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimmi, Edward R
 REGISTRATION NUMBER: 38, 891
 REFERENCE/DOCKET NUMBER: P31624
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; MOLECULE TYPE: protein
 ; US-09-183-134-2

Query Match Similarity 5.1%; Score 108; DB 4; Length 197;
 Best Local Similarity 25.3%; Pred. No. 0.00067; Mismatches 73; Indels 24; Gaps 6;
 Matches 42; Conservative 27; MisMatches 73; Indels 24; Gaps 6;

Qy 237 IPCATDODPYRMRTRD-----VAPRIGYPKPALLHSPPALQGAOTKMSA 282
 Db 5 VPGVGTQPKPMIBQTRBIVRSFNNAVNCDVLVPEEGIYIPENE--RAGRLPGLDG-NAKMSK 61

Qy 283 SDPNSSIFLTDTAKOIKTKVVKHAFSGGRDTIEBRHQFGNCNDVSVFMYLTF--LEDD 340
 Db 62 S-LNNGIYLADDATLTKVMSMTPDHIREVPEKIEGN---MVFHYLDVGRPEDA 116

Qy 341 DKLEQTRKDVTSGAMLTGELKKALIEVQLAEHQARKEVTDI 386
 Db 117 QEIADMKERYORGGLGDVKTKYVLLERELGPIRRERRFAKM 162

RESULT 13
 US-09-183-134-2
 Sequence 2, Application US/09183134
 Patent No. 6165759

GENERAL INFORMATION:
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: NOVEL TRYPTOPHANYL tRNA
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0939

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/183, 134
 FILING DATE:
 CLASSIFICATION:
 PRIORITY INFORMATION:
 APPLICATION NUMBER: 08/923, 867
 FILING DATE: 04-SEP-1997
 APPLICATION NUMBER: 9619072..3
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimmi, Edward R
 REGISTRATION NUMBER: 38, 891
 REFERENCE/DOCKET NUMBER: P31624
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; MOLECULE TYPE: protein
 ; US-09-183-134-2

GenCore version 5.1.6
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OM protein - protein search, using sw model:

Run on: July 10, 2003, 12:24:54 ; Search time 32.08 Seconds
Sequence: 1 SNHGDPDATEAEEDFVDPWTY.....VTEIVKEMTPRKLSPDFQ 401
1665.633 Million cell updates/sec

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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3: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1982.DAT:*

4: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1983.DAT:*

5: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1984.DAT:*

6: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1985.DAT:*

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11: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1990.DAT:*

12: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1991.DAT:*

13: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1992.DAT:*

14: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA1993.DAT:*

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22: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA2001.DAT:*

23: /SIDB2/gcdata/geneseq/geneseqP-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match Length	DB ID	Description
1	2116	100.0	415 22 AAB47617	Human supermini Trp
2	2116	100.0	415 23 AAE13493	Human supermini trp
3	2116	100.0	437 22 AAB47616	Human mini Trp top
4	2116	100.0	437 23 AAE13492	Human full-length Trp
5	2116	100.0	484 22 AAB47615	Human tryptophanyl
6	2116	100.0	484 23 AAE13491	Lung cancer associ
7	2101	99.3	475 21 AAB58220	Human HCV inducib
8	2096	99.1	471 20 AAY05372	Human inactive Trp
9	1988	94.0	392 22 AAB47618	Human inactive Trp
10	1988	94.0	392 23 AAE13494	Human inactive Trp

ALIGNMENTS

RESULT 1
ID AAB47617
XX AAB47617 standard; Protein; 415 AA.
AC AAB47617;
XX DT 07-JAN-2002 (first entry)
XX DE Human supermini Trps.
XX KW Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trprS; vascular graft surgery.
XX OS Homo sapiens.
XX PN WO200174811-A1.
XX PD 11-OCT-2001.
XX PF 21-MAR-2001; 2001WO-US08966.
XX PR 31-MAR-2000; 2000US193471P.
XX (SCRI) SCRIPPS RES INST.
XX PI Schimmel P, Wakasugi K;
XX DR WPI; 2001-626377/72.
DR N-PSDB; AAH43604.

11 1370.5 64.8 430 22 ABB64621 Drosophila melanog
12 1370.5 64.8 430 22 ABB67203 Drosophila melanog
13 1304 61.6 426 21 AAG23697 Arabidopsis thaliana
14 1304 61.6 426 21 AAG23697 Arabidopsis thaliana
15 1218.5 57.6 424 22 AAB65931 Tryptophanyl-tRNA
16 96.8 45.7 292 21 AAG23699 Arabidopsis thaliana
17 83.1 39.3 173 21 AAB58517 Lung cancer associ
18 80.3 37.9 385 22 AAB58609 Putative P. abyssi
19 32.8 15.5 23 AAE13515 Human tryptophanyl
20 226.5 10.7 142 21 AAB58719 Lung cancer associ
21 203.5 9.6 341 23 ABB26964 Streptococcus poly
22 185.5 8.8 341 19 AAW56423 Tryptophanyl tRNA
23 185.5 8.8 341 22 AAU38511 Streptococcus pneu
24 182.5 8.6 341 23 ABB26965 Streptococcus poly
25 174.5 8.2 341 23 ABB53366 Lactococcus lactic
26 164.5 7.8 409 20 AAW94248 C. albicans tyrosy
27 162.5 7.7 409 20 AAW94247 Protein involved i
28 159.5 7.5 379 20 AAY77623 Putative P. abyssi
29 158.5 7.5 378 22 ABB96600 Chamydia pneumoniae
30 152 7.2 344 20 AAY35439 Human mini tyrosyl
31 147 6.9 345 23 AAE13516 Helicobacter pylor
32 146 6.9 339 22 AAU35829 Human mini tyrosyl
33 138.5 6.5 140 21 AAG23032 Arabidopsis thalia
34 134.5 6.4 22 ABB6745 Drosophila melanog
35 134 6.3 372 22 ABB47614 Human mini tyrosyl m
36 134 6.3 372 23 AAE13490 Human mini tyrosyl
37 132.5 6.3 372 23 AAE137612 Human mini tyrosyl
38 132.5 6.3 372 23 AAE13488 Human mini tyrosyl
39 132.5 6.3 536 22 AAB47611 Human full length
40 132.5 6.3 536 23 AAE13487 Human tyrosyl t-RN
41 128 6.0 334 22 AAU35477 Haemophilus influe
42 126.5 6.0 419 23 ABB49417 Listeria monocytog
43 123 5.8 347 21 AAG31904 Aradopsis thalia
44 122.5 5.8 346 21 AAG48617 Human tyrosyl
45 119 5.6 415 23 AAU79165 Human tyrosyl-tRNA

Db 122 LVIQMTDBKYLWKLDTLDQAYGDAVENAKDITACGFDDINKTFPSFSDIYMGMSGYKN 181
 CC for cosmetic purposes. It is particularly useful in the treatment of
 CC abdominal wounds where there is high risk of infection. Truncated Trprs
 CC promotes endothelialization in vascular graft surgery and is used in
 CC conjunction with angiography to administer the angiogenic tRNA
 CC synthetase polypeptides or polymucleotides directly to the lumen and
 CC wall of the blood vessel.

Db 182 VVKIQKETVFNQVKGIFGFTSDCIGKISFPQIAQPSFSMSPPQIFRDRDIDQCMPCA 240
 CC SQ Sequence 437 AA:

Query Match 100.0%; Score 2116; DB 22; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFPALQACTNSASDPNNSIFLTDAQIKT 300
 CC Sq 1 SNHGPDATEABEDFVDPWTWOTSSAKGIDYKLTVRGSSKIDKLINRERATGCPHRH 60
 Db 302 KVNKAHSGGRTIEHRQFGCNCUDVSFMYLTFLEDDDKLQEQRKDVTSGAMLTGEL 361
 CC Sq 24 SNHGPDATEABEDFVDPWTWOTSSAKGIDYKLTVRGSSKIDKLINRERATGCPHRH 83
 Db 361 KKALIEVLQPLIAEHOARRKEVTDIVKEFMPRKLSFDQ 401
 CC Sq 61 FLRGGFPSHRDMQVLDAYENKKPYLYTGRGSEAMVGHJIPRFYKALQVNTP 120
 Db 362 KKALIEVLQPLIAEHOARRKEVTDIVKEFMPRKLSFDQ 402
 CC Sq 84 FLRRGFFPSHRDMQVLDAYENKKPYLYTGRGSEAMVGHJIPRFYKALQVNTP 143
 Db 121 LVIQMTDDBEKYLWKLDTLDQAYGDAVENAKDITACGFDDINKTFPSFSDIYMGMSGYKN 180
 CC Sq 144 LVIQMTDDBEKYLWKLDTLDQAYGDAVENAKDITACGFDDINKTFPSFSDIYMGMSGYKN 203
 Db 181 VVKIQKETVFNQVKGIFGFTSDCIGKISFPQIAQPSFSMSPPQIFRDRDIDQCMPCA 240
 CC Sq 204 VVKIQKETVFNQVKGIFGFTSDCIGKISFPQIAQPSFSMSPPQIFRDRDIDQCMPCA 263
 Db 264 IDQDPYFRMTRDVAPRIGYPKPALLHSTFPALQACTNSASDPNNSIFLTDAQIKT 323
 CC Sq 241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFPALQACTNSASDPNNSIFLTDAQIKT 300
 Db 301 KVNKAHSGGRTIEHRQFGCNCUDVSMSMFLPLEDDDKLQEQRKDVTSGAMLTGEL 360
 CC Sq 324 KVNKAHSGGRTIEHRQFGCNCUDVSMSMFLPLEDDDKLQEQRKDVTSGAMLTGEL 383
 Db 361 KKALIEVLQPLIAEHOARRKEVTDIVKEFMPRKLSFDQ 401
 CC Sq 384 KKALIEVLQPLIAEHOARRKEVTDIVKEFMPRKLSFDQ 424

RESULT 3

ID AAB47616 standard; Protein: 437 AA.
 AC AAB47616;
 XX DT 07-JAN-2002 (first entry)
 DE Human mini Trprs.
 XX TyrSyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain;
 KW vascular endothelial cell function; burn; plastic surgery; abdomen;
 KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
 KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;
 KW dermal ulcer; diabetic ulcer; endothelialization;
 KW triptophanyl-tRNA synthetase; trprs; vascular graft surgery.
 XX Homo sapiens.
 XX WO200174841-A1.
 PD 11-OCT-2001.
 XX PP 21-MAR-2001; 2001WO-US08966.
 PR 31-MAR-2000; 2000US-193471P.
 XX PA (SCRIP) SCRIPPS RES INST.
 XX PI Schimmel P, Wakasugi K;
 XX DR N-PSDB; AAH43603.
 XX PT New human truncated tyrosyl-tRNA synthetase polypeptide for regulating
 PT vascular endothelial function, in particular for regulating
 PT angiogenesis, tumor metastasis, and treating myocardial infarction -
 XX PS Disclosure, Page 123-24; 150pp; English.
 CC The sequences given in AAB47615-18 show full length and truncated
 CC versions of triptophanyl-tRNA synthetase (Trprs). The truncated Trprs of
 CC the invention comprises a Rossmann fold nucleotide binding domain, and
 CC is capable of regulating vascular endothelial cell function. It is of
 approx. 40 kilo Dalton molecular weight and is produced by cleavage of truncated
 CC full length Trprs with polymorphonuclear leucocyte elastase. Truncated
 CC Trprs is useful for regulating angiogenesis, tumor metastasis,
 CC enhancing angiogenesis to a graft, treating myocardial infarction,
 CC solid tumor, and a condition that would benefit from increased or
 CC decreased angiogenesis in a mammal, in particular humans. It is also
 CC useful in diagnosis and as a wound healing agent for treating wounds
 CC such as dermal ulcers, diabetic ulcers, burns and injuries and in
 CC plastic surgery when reconstruction is required following a burn or

RESULT 4

ID AAE13492 standard; Protein: 437 AA.
 AC AAE13492;
 PA XX DT 12-FEB-2002 (first entry)
 DE Human mini triptophanyl t-RNA synthetase in PET20B.
 XX Human; triptophanyl-tRNA synthetase; Trprs; tyrosyl t-RNA synthetase;
 KW Trprs; vascular endothelial cell function; angiogenesis; wound healing;
 KW re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;
 KW diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;
 KW angiography; gene therapy; tumour; inflammation; vascular permeability;
 KW rheumatoid arthritis; psoriasis; diabetic retinopathy.
 XX OS Homo sapiens.
 XX PN WO200175078-A1.
 PR 11-OCT-2001.
 XX PF 21-MAR-2001; 2001WO-US08975.
 PR 31-MAR-2000; 2000US-193471P.
 PA (SCRIP) SCRIPPS RES INST.
 XX PI Schimmel P, Wakasugi K;
 XX

DR WPI; 2002-010784/01.
 DR N-PSDB; AAB22483.
 XX
 PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of
 PT regulating vascular endothelial cell function, preferably angiogenesis,
 PT is useful for treating solid tumor or suppressing tumor metastasis in
 PT mammal -
 XX
 PS Example 1; Page 123-124, 149pp; English.
 XX
 CC The patient discloses human aminoacyl tRNA synthetases, particularly
 CC truncated tryptophanyl-tRNA synthetases (TrPRS) comprising a Rossmann
 CC fold nucleotide binding domain and polynucleotides encoding them. The
 CC invention also relates to tyrosyl t-RNA synthetases (TyRS). TrPRS
 CC sequences are useful for regulating vascular endothelial cell function,
 CC preferably angiogenesis. Angiogenic TrPRS sequences are useful as wound
 CC healing agents for re-vascularising damaged tissues. They are useful for
 CC treating full-thickness wounds (e.g. dermal ulcers, including pressure
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrPRS
 CC sequences can also be used in plastic surgery when reconstruction is
 required following a burn, other trauma, or even for cosmetic purposes.
 CC Angiogenic TrPRS is also used in association with surgery and following
 CC the repair of cuts, for promoting endothelialization in vascular graft
 CC surgery and for repairing the damage of myocardial infarction and in
 CC conjunction with coronary bypass surgery by stimulating the growth of
 CC transplanted tissue. TrPRS is also used in conjunction with angiography.
 CC TrPRS DNAs are useful in gene therapy. TrPRS antibodies are used in
 CC immunoassays to detect the presence of tumours. They are also useful
 CC for blocking endogenous angiogenic activity and retard the growth of
 CC solid tumours. These antibodies may also be used to treat inflammation
 CC caused by increased vascular permeability. Inhibiting the activity of
 CC TrPRS by antisense technology is useful for preventing further growth
 CC or even regress solid tumours, and for treating rheumatoid arthritis,
 CC psoriasis, diabetic retinopathy, all of which are characterized by
 CC abnormal angiogenesis. The present sequence is human truncated
 CC tryptophanyl t-RNA synthetase (mini TrPRS; residues 48-471 of
 CC full-length TrPRS protein) protein in PET2B.
 XX
 SQ Sequence 437 AA;

SQ

Score 2116; DB 23; Length 437;

RESULT 5

RAB47615

ID AAB47615 standard; Protein; 484 AA.

XX

AC AAB47615;

XX

DT 07-JAN-2002 (first entry)

XX

DE Human full-length TrPRS.

XX

KW Tyrosyl-tRNA synthetase; TyRS; Rossmann fold nucleotide binding domain;

KW vascular endothelial cell function; burn; plastic surgery; abdomen;

KW polyphosphonucleic leucocyte elastase; angiogenesis; tumour metastasis;

KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;

KW dermal ulcer; diabetic ulcer; endothelialization; graft surgery.

XX

OS Homo sapiens.

XX

PN WO200174841-A1.

XX

PR 11-OCT-2001.

XX

PA 21-MAR-2001; 2001WO-US08966..

XX

PR 31-MAR-2000; 2000US-193471P.

XX

PA (SCRIP) SCRIPPS RES INST.

XX

PI Schimmel P; Wakasugi K;

XX

PT WPI; 2001-626377/72.

XX

DR N-PSDB; AAB43602.

XX

PR New human truncated tyrosyl-tRNA synthetase polypeptide for regulating

CC vascular endothelial function, in particular for regulating myocardial infarction

XX

RS disclosure; Page 117-19; 150pp; English.

XX

CC The sequences given in AAB47615-18 show full length and truncated

CC versions of tryptophanyl-tRNA synthetase (TrPRS). The truncated TrPRS of

CC the invention comprises a Rossmann fold nucleotide binding domain and

CC is capable of regulating vascular endothelial cell function. It is of

CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of

CC full length TrPRS with polyphosphonucleic leucocyte elastase. Truncated

CC TrPRS is useful for regulating angiogenesis, tumor metastasis,

CC enhancing angiogenesis to a graft, treating myocardial infarction,

CC solid tumor, and a condition that would benefit from increased or

CC decreased angiogenesis in a mammal, in particular humans. It is also

CC useful in diagnosis and as a wound healing agent for treating wounds

CC such as dermal ulcers, diabetic ulcers, burns and injuries and in

CC plastic surgery when reconstruction is required following a burn or

CC for cosmetic purposes. It is particularly useful in the treatment of

CC abdominal wounds where there is high risk of infection. Truncated TrPRS

CC promotes endothelialization in vascular graft surgery and is used in

CC conjunction with angiography to administer the angiogenic tRNA

CC synthetase polypeptides or polynucleotides directly to the lumen and

CC wall of the blood vessel.

XX

SQ Sequence 484 AA;

SQ

Query Match 100.0%; Score 2116; DB 22; Length 484;

Best Local Similarity 100.0%; Pred. No. 2.1e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNMGPDATEAEEDFDVPMWVOTSAKGDYDYLKLVFGRSSKKIDKEILNIRATGQRPHH 60

Db 24 SNHGPDATEAEEDFDVPMWVOTSSAKGDYDYLKLVFGRSSKKIDKEILNIRATGQRPHH 83

Qy 61 FLRRGIFFSHRDMNQVLDAYENKKPFVLYTGRGPSSSEAMHGHLIPIFTKWLQDVFNVP 120

Db 84 FLRRGIFFSHRDMNQVLDAYENKKPFVLYTGRGPSSSEAMHGHLIPIFTKWLQDVFNVP 143

Qy 121 LVIQMTDDEBKYLWKLDTLQDAVGAVAKDIAAGFDINKITFSDLYMMSGYTKN 180

Db 144 LVIQMTDDEBKYLWKLDTLQDAVGAVAKDIAAGFDINKITFSDLYMMSGYTKN 203

Qy 181 VVKIQKHYTFNQVKGIGFPTSDCIGKLSFPATOQAPSNSNSTQIFDRDTQCLPCA 240

Db 204 VKLQKHTFNFQVKGIGFPTSDCIGKLSFPATOQAPSNSNSTQIFDRDTQCLPCA 263

Qy 241 IDDPYFRTRDVAPIRGYPKALLHSPPALQAGAQTESSASPDNPNSIFLDTAKQT 300

Db 264 IDDPYFRTRDVAPIRGYPKALLHSPPALQAGAQTESSASPDNPNSIFLDTAKQT 323

Qy 301 KVKHAFSGGRDTIEHHQFGNCDDYFSPMLPFLDDDKLEQIRDYTSQAMLGTL 360

Db 324 KVKHAFSGGRDTIEHHQFGNCDDYFSPMLPFLDDDKLEQIRDYTSQAMLGTL 383

Qy 361 KAKLIEVQPLIAHQARKEVDEIVKEFMPKLSDFQ 401

Db 384 KAKLIEVQPLIAHQARKEVDEIVKEFMPKLSDFQ 424

Qy 1 SNMGPDATEAEEDFDVPMWVOTSAKGDYDYLKLVFGRSSKKIDKEILNIRATGQRPHH 60

Db 71 SNMGPDATEAEEDFDVPMWVOTSSAKGDYDYLKLVFGRSSKKIDKEILNIRATGQRPHH 130

Qy 61 FLRRGIFFSHRDMNQVLDAYENKKPFVLYTGRGPSSSEAMHGHLIPIFTKWLQDVFNVP 120

Db 131 FLRRGIFFSHRDMNQVLDAYENKKPFVLYTGRGPSSSEAMHGHLIPIFTKWLQDVFNVP 190

required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TRPs is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TRPs is also used in conjunction with angiogenesis. TRPs DNAs are useful in gene therapy. TRPs antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TRPs by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human tryptophanyl t-RNA synthetase (TRPs) in pET20B.

XX	PP	08-MAR-2000; 2000WO-US05918.
PR	12-MAR-1999; 99US-0124270.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PA	(ROSE/) ROSEN C A.
PT	Ruben SM;	
XX	DR	WPI; 2000-597514/55.
XX	DR	N-PSDB; AAF18096.
PT	lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -	
PT	lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -	
PS	Claim 11; Page 1052-1053; 1425pp; English.	
XX	CC	Polymerotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polymerotide sequences, their agonists, and antagonists, may have neuroprotective; cytotoxic; cardioactive; immunomodulatory; muscular active general; pulmonary; gastrointestinal activity; nephrotoxic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polymerotide sequences. The lung cancer associated polymerotide sequences may be used for detection of lung cancer, chromosome identification, as chromosomal markers, and for numerous other diagnostic or research purposes. The protein may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polymerotide sequences AAF18425 - AAF18433 and peptide AAB8549 are used in the course of the invention for the identification and characterisation of the polymerotide and protein sequences.
XX	CC	Best Local Similarity 99.5%; Pred. No. 7.1e-208; Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 60
OY	75	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 134
Db	61	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 120
Db	135	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 194
QY	121	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIAGCDFINKTFPSLDDYGMGSSGYKN 180
QY	195	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIAGCDFINKTFPSLDDYGMGSSGYKN 254
OY	181	WVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 240
OY	255	VVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 314
Db	241	IDQDPYFRMTRDVARIGYKPALKHSTFPALQAOQTKMSASDNNPSLFTDPAQIKT 300
QY	315	IDQDPYFRMTRDVARIGYKPALKHSTFPALQAOQTKMSASDNNPSLFTDPAQIKT 374
OY	301	KVNKHAFSGQRDTIEBHRQFGGNCDVDFMLTFFLEDDKLGEOIRKDYTGAMLGEL 360
Db	375	KVNKHAFSGQRDTIEBHRQFGGNCDVDFMLTFFLEDDKLGEOIRKDYTGAMLGEL 434
QY	361	KKALIEVLOPLIAHQARKEVTEBVKEMTPRKLSDFQ 401
Db	435	KKALIEVLOPLIAHQARKEVTEBVKEMTPRKLSDFQ 475
PS	Sequence 475 AA;	
XX	CC	Query Match 99.3%; Score 2101; DB 21; Length 475; Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 60
OY	75	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 134
Db	61	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 120
Db	135	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 194
QY	121	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIAGCDFINKTFPSLDDYGMGSSGYKN 180
QY	195	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIAGCDFINKTFPSLDDYGMGSSGYKN 254
OY	181	WVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 240
OY	255	VVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 314
Db	241	IDQDPYFRMTRDVARIGYKPALKHSTFPALQAOQTKMSASDNNPSLFTDPAQIKT 300
QY	315	IDQDPYFRMTRDVARIGYKPALKHSTFPALQAOQTKMSASDNNPSLFTDPAQIKT 374
OY	301	KVNKHAFSGQRDTIEBHRQFGGNCDVDFMLTFFLEDDKLGEOIRKDYTGAMLGEL 360
Db	375	KVNKHAFSGQRDTIEBHRQFGGNCDVDFMLTFFLEDDKLGEOIRKDYTGAMLGEL 434
QY	361	KKALIEVLOPLIAHQARKEVTEBVKEMTPRKLSDFQ 401
Db	435	KKALIEVLOPLIAHQARKEVTEBVKEMTPRKLSDFQ 475
PS	Sequence 475 AA;	
XX	CC	Query Match 99.1%; Score 2096; DB 20; Length 471; Best Local Similarity 99.3%; Pred. No. 2.3e-207; Matches 398; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	1	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 60
OY	71	SNHGPDATAEEDFDVDPWTVQTSASSAKGIDKIDKLIRFRGSSKIDKEILNRRATRGRPHH 130
Db	61	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 120
Db	131	FLRRGGIFFSHRDMDNQVLDAYENKKPFLYTRGRGSSEAMVGHLLPFITKWLDQDVFNVP 190
QY	121	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIACGFDINKTFPSLDDYGMGSSGYKN 180
Db	191	LVIQMDDEDKYLWKDQTLTDQAYGDRAVENAKDIIACGFDINKTFPSLDDYGMGSSGYKN 250
OY	181	WVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 240
Db	251	WVKICKHVKVFNQVKGIGFSDCIGKISPAIQAPSNSNFSFQIFRRTDQCLIPCA 310
QY	241	IDQDPYFRMTRDVARIGYKPALKHSTFPALQAOQTKMSASDNNPSLFTDPAQIKT 300

CC truncated tryptophanyl-tRNA synthetases (TrPRs) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to tyrosyl-tRNA synthetases (TyRS). TrPRs sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrPRs sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers), including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrPRs sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrPRs is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrPRs is also used in conjunction with angiography. TrPRs DNAs are useful in gene therapy. TrPRs antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumour. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrPRs by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human inactive CC tryptophanyl t-RNA synthetase (TrPRs) in pET20B.

XX Sequence 392 AA;

Query Match 94.0%; Score: 1988; DB 23; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.5e-16; Mismatches 0; Indels 0; Gaps 0; Matches 378; Conservative 0;

Oy 24 SAKGKIDYDVKLIVRGSSKIDKEKLINIERATGORPHFLRRGGFFSHRDMDNQVDAENK 83
Db 2 SAKGKIDYDVKLIVRGSSKIDKEKLINIERATGORPHFLRRGGFFSHRDMDNQVDAENK 61

Qy 84 KPPFLYTGRGPSSSEAMVHGLIPLIFTKMQLQDVENVPLVQMTDEKLWQDOLTDQNG 143
Db 62 KPPFLYTGRGPSSSEAMVHGLIPLIFTKMQLQDVENVPLVQMTDEKLWQDOLTDQNG 121

Qy 144 DAVENAKOJIACGFDINKTFTPSLDYDMMSGGYKVNVKIQEVNTFQVK3TFGGFTSD 203
Db 122 DAVENAKOJIACGFDINKTFTPSLDYDMMSGGYKVNVKIQEVNTFQVK3TFGGFTSD 181

Qy 204 CTGKISFPQIAQPSFSNSPSPQIFDRDTCIQCIPCAIDODPYFRMTRDVAAPRIGPKA 263
Db 182 CTGKISFPQIAQPSFSNSPSPQIFDRDTCIQCIPCAIDODPYFRMTRDVAAPRIGPKA 241

Qy 264 LASHTEPPALQAGTOKMSASPDNSIPLTDTAKOIKTKNKAHPSGADTIEHHRQGNN 323
Db 242 LASHTEPPALQAGTOKMSASPDNSIPLTDTAKOIKTKNKAHPSGGRDTIEBHRQGNN 301

Qy 324 CDDVDSFMUFTFLADDKLEQIRKDQYTSQAGMLTGELKKALLEVLQPLIAHQARKKET 383
Db 302 CDDVDSFMUFTFLADDKLEQIRKDQYTSQAGMLTGELKKALLEVLQPLIAHQARKKET 361

Qy 384 DEIVKEFMPTRKUSFDFQ 401
Db 362 DEIVKEFMPTRKUSFDFQ 379

RESULT 11

ABB64621 DT 26-MAR-2002 (first entry)

XX ID ABB64621 standard; Protein; 430 AA.

XX AC ABB64621;

XX KW Drosophila melanogaster polypeptide SEQ ID NO 20655.

XX pharmacetical.

XX Drosophila melanogaster.

OS XX WO200171042-A2.

PN XX 27-SEP-2001.

PR XX 23-MAR-2001; 2001WO-US09231..

PR XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA XX (PEKE) PE CORP NY.

PA XX Venter JC, Adams M, Li PWD, Myers EW;

PA XX DR N-PSDB; AB108724.

PA XX WPI; 2001-656860/75.

PA XX Venter JC, Adams M, Li PWD, Myers EW;

PA XX DR N-PSDB; AB108724.

PA XX WPI; 2001-656860/75.

PA XX Disclosure: SEQ ID NO 20655; 21PP + Sequence Listing; English.

XX Sequence 430 AA;

Query Match 64.8%; Score: 1370.5; DB 22; Length 430;
Best Local Similarity 64.5%; Pred. No. 1.7e-132; Mismatches 23; Indels 1; Gaps 1; Matches 253; Conservative 62;

Oy 7 ATAAEAEFDVDPWTVQSSAKGKIDYDVKLIVRGSSKIDKEKLINIERATGORPHFLRRGI 66
Db 38 ATAAEAEFDVDPWTVQSSAKGKIDYDVKLIVRGSSKIDKEKLINIERATGORPHFLRRGI 97

Oy 67 FSHRDMDNQVDAENKPPFLYTGRGPSSSEAMVHGLIPLIFTKMQLQDVENVPLVQMT 126
Db 98 FSHRDMDNQVDAENKPPFLYTGRGPSSSEAMVHGLIPLIFTKMQLQDVENVPLVQMT 157

Oy 127 DDKTLYWQDUTDQYDAENKADIACGFDINKTFTPSLDYDMMSGGYKVNVKIQEVNTFQVK 186
Db 158 DDKTLYWQDUTDQYDAENKADIACGFDINKTFTPSLDYDMMSGGYKVNVKIQEVNTFQVK 217

Oy 187 HUTPNQVKGIRGFTDSCIGKISFPQIAQPSFSNSPSPQIFDRDTCIQCIPCAIDODPY 246
Db 218 CUVFNQVKGIRGFTDSCIGKISFPQIAQPSFSNSPSPQIFDRDTCIQCIPCAIDODPY 276

Oy 247 FRMTRDVAAPRIGPKPALHSTFFPALLQGAQTMKSASPDNSIIFLTDTAKOIKTKNKA 306
Db 277 FRMTRDVAAPRIGPKCALHSITFFPALLQGAQTMKSASPDNSIIFLTDTAKOIKTKNKA 336

Oy 307 FSGGRDTTEERHQFGGMCDVDFMVLTFPLDDDKLEQIRKDQYTSQAGMLTGELKKALLE 366
Db 337 FSGGRDTTEERHQFGGMCDVDFMVLTFPLDDDKLEQIRKDQYTSQAGMLTGELKKALLE 396

Oy 367 VIQPLIAHQARKKETDDEIVKEFMPTRKUSFDFQ 398
Db 397 TUPPIVSGHQARKLITDEVLQPLIAHQARKKETDDEIVKEFMPTRKUSFDFQ 428

RESULT 12

QY	307	PSSGRGOTIEERHROFGCNCMVMSFLTTEFDDKLEQIRKDYTSGAMILTGELKKALIE
ID	ABB67203	standard; Protein; 430 AA.
XX	XX	
AC	AC	
ABB67203;		
XX		
DT	26-MAR-2002	(first entry)
XX		
DE	Drosophila melanogaster polypeptide SEQ ID NO 28401.	
XX		
KW	Drosophila; developmental biology; cell signalling; insecticide;	
KW	pharmaceutical.	
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PP	23-MAR-2001; 2001WO-US029231.	
XX		
PR	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-0614150.	
XX		
PA	(PERKE) PE CORP NY.	
XX		
PT	Venter JC, Adams M, Li PW, Myers EW;	
XX		
DR	WPI; 2001-656860/75.	
XX		
DR	N-PSSDB; ABL11306.	
XX		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	
PT	Disclosure; SEQ ID NO 28401; 21pp + Sequence Listing; English.	
PS	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL7737-ABL72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
CC	CC	
SQ	Sequence 430 AA;	
Query Match	64.8%	Score 1370.5; DB 22; Length 430;
Best Local Similarity	64.5%	Pred. No. 1.7e-132;
Matches	253;	Conservative 62; Mismatches 76; Indels 1; Gaps 1;
QY	7	ATREABEDFDWPWTQVTSAXKGIDIKLIVRGSSKIDKEIJNFRATGPHPHLRGGI 66
Db	3.8	ATAPPEDFDWPWTQVTSAXKGIDIKLIVRGSSKIDKEIJNFRATGPHPHLRGGI 97
QY	67	FPSHRDMNOVTDAYRNKPKPYLYTRGSPSSAMHGHLLIPITFTKMLQDVNPVNUVQMT 126
Db	98	FPSHRDLHTILTRRQKPKPYLYTRGSPSSALHGHLLIPITFTKMLQDVNPVNUVQMT 157
QY	127	DDEKYLWKDQLTDQYDAGDENAKOIAACSPDINCPFIERSLDYMGMSSFYKVNWKICK 186
Db	158	DDEKYLWKDQLKVEDAIIKGRENNAOKIVAIAGFDVNKPFIFNNEFVGKCPAMYONIRIOK 217
QY	187	HVTFRQVKGIGFGFTPSDCIGKISFFAIQAAPSFSNSFPQIFRDRDTRDIQCLIPCAIQDQPY 246
Db	218	CVTFENQVKGIGFGFTPSDCIGKISFFAIQAAPSFSNSFPQIFRDRDTRDIQCLIPCAIQDQPY 276
247	FRMFTDVAPIRGFPCCALINSTFFPALQGAKTNKRSADQNSAVYLJDTPKQIKNNKLYKA 306	
QY	277	FRMFTDVAPIRGFPCCALINSTFFPALQGAKTNKRSADQNSAVYLJDTPKQIKNNKLYKA 336
QY	307	PSSGRGOTIEERHROFGCNCMVMSFLTTEFDDKLEQIRKDYTSGAMILTGELKKALIE
ID	AAG23698	standard; Protein; 402 AA.
XX		
AC	AAG23698;	
XX		
DT	17-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 27101.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PP	25-FEB-2000; 2000EP-0301439.	
XX		
PR	25-FEB-1999; 99US-0121825.	
PR	05-MAR-1999; 99US-0123180.	
PR	09-MAR-1999; 99US-0123548.	
PR	23-MAR-1999; 99US-0123788.	
PR	25-MAR-1999; 99US-0126264.	
PR	29-MAR-1999; 99US-0126785.	
PR	01-APR-1999; 99US-0127462.	
PR	06-APR-1999; 99US-0128234.	
PR	08-APR-1999; 99US-0128714.	
PR	16-APR-1999; 99US-0128845.	
PR	19-APR-1999; 99US-0130077.	
PR	21-APR-1999; 99US-0130449.	
PR	23-APR-1999; 99US-0130510.	
PR	28-APR-1999; 99US-0130449.	
PR	30-APR-1999; 99US-0130048.	
PR	04-MAY-1999; 99US-0130449.	
PR	05-MAY-1999; 99US-0132485.	
PR	06-MAY-1999; 99US-0132486.	
PR	07-MAY-1999; 99US-0132863.	
PR	11-MAY-1999; 99US-013256.	
PR	14-MAY-1999; 99US-0134218.	
PR	14-MAY-1999; 99US-0134219.	
PR	14-MAY-1999; 99US-0134221.	
PR	14-MAY-1999; 99US-0134370.	
PR	18-MAY-1999; 99US-0134768.	
PR	19-MAY-1999; 99US-0134941.	
PR	20-MAY-1999; 99US-0135124.	
PR	21-MAY-1999; 99US-0135353.	
PR	24-MAY-1999; 99US-0135229.	
PR	25-MAY-1999; 99US-0136021.	
PR	27-MAY-1999; 99US-0136392.	
PR	28-MAY-1999; 99US-0136782.	
PR	01-JUN-1999; 99US-0137222.	
PR	03-JUN-1999; 99US-0137528.	
PR	04-JUN-1999; 99US-0137502.	
PR	07-JUN-1999; 99US-0137744.	
PR	08-JUN-1999; 99US-0138094.	
PR	10-JUN-1999; 99US-0138540.	

PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148411.
PR	17-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	18-JUN-1999;	99US-0139454.	PR	13-AUG-1999;	99US-0148844.
PR	18-JUN-1999;	99US-0139455.	PR	15-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139456.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139457.	PR	18-AUG-1999;	99US-0149326.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149939.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150366.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151080.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151089.
PR	24-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151338.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151330.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0151066.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	02-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	05-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155300.
PR	08-JUN-1999;	99US-0142803.	PR	10-SEP-1999;	99US-0155358.
PR	09-JUL-1999;	99US-0142920.	PR	15-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156556.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143542.	PR	05-OCT-1999;	99US-0157553.
PR	19-JUL-1999;	99US-0144332.	PR	06-OCT-1999;	99US-0157866.
PR	19-JUL-1999;	99US-0144333.	PR	07-OCT-1999;	99US-0158059.
PR	16-JUL-1999;	99US-0144005.	PR	28-SEP-1999;	99US-0158232.
PR	16-JUL-1999;	99US-0144085.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144325.	PR	13-OCT-1999;	99US-0159233.
PR	19-JUL-1999;	99US-0144331.	PR	14-OCT-1999;	99US-0159637.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159924.
PR	19-JUL-1999;	99US-0144333.	PR	14-OCT-1999;	99US-0159925.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159339.
PR	19-JUL-1999;	99US-0144335.	PR	08-OCT-1999;	99US-0158232.
PR	20-JUL-1999;	99US-0144352.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144632.	PR	13-OCT-1999;	99US-0159233.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	13-OCT-1999;	99US-0159924.
PR	21-JUL-1999;	99US-0144814.	PR	14-OCT-1999;	99US-0159925.
PR	21-JUL-1999;	99US-0144814.	PR	14-OCT-1999;	99US-0159339.
PR	21-JUL-1999;	99US-0145086.	PR	14-OCT-1999;	99US-0159339.
PR	21-JUL-1999;	99US-0145088.	PR	14-OCT-1999;	99US-0159339.
PR	22-JUL-1999;	99US-0145085.	PR	14-OCT-1999;	99US-0159339.
PR	22-JUL-1999;	99US-0145085.	PR	14-OCT-1999;	99US-0159339.
PR	22-JUL-1999;	99US-0145087.	PR	14-OCT-1999;	99US-0159637.
PR	22-JUL-1999;	99US-0145087.	PR	14-OCT-1999;	99US-0159637.
PR	22-JUL-1999;	99US-0145089.	PR	14-OCT-1999;	99US-0159637.
PR	22-JUL-1999;	99US-0145089.	PR	14-OCT-1999;	99US-0159637.
PR	22-JUL-1999;	99US-0145192.	PR	14-OCT-1999;	99US-0159637.
PR	22-JUL-1999;	99US-0145145.	PR	14-OCT-1999;	99US-0159637.
PR	23-JUL-1999;	99US-0145218.	PR	21-OCT-1999;	99US-0160767.
PR	23-JUL-1999;	99US-0145224.	PR	21-OCT-1999;	99US-0160768.
PR	26-JUL-1999;	99US-0145276.	PR	21-OCT-1999;	99US-0160770.
PR	27-JUL-1999;	99US-0145913.	PR	21-OCT-1999;	99US-0160814.
PR	27-JUL-1999;	99US-0145913.	PR	21-OCT-1999;	99US-0160815.
PR	27-JUL-1999;	99US-0145918.	PR	22-OCT-1999;	99US-0160940.
PR	27-JUL-1999;	99US-0145918.	PR	22-OCT-1999;	99US-0160940.
PR	28-JUL-1999;	99US-0145919.	PR	22-OCT-1999;	99US-0160940.
PR	28-JUL-1999;	99US-0145919.	PR	22-OCT-1999;	99US-0160940.
PR	04-AUG-1999;	99US-0145951.	PR	22-OCT-1999;	99US-0160940.
PR	05-AUG-1999;	99US-0147302.	PR	22-OCT-1999;	99US-0160940.
PR	05-AUG-1999;	99US-0147260.	PR	23-OCT-1999;	99US-0161404.
PR	05-AUG-1999;	99US-0147303.	PR	23-OCT-1999;	99US-0161405.
PR	06-AUG-1999;	99US-0147416.	PR	25-OCT-1999;	99US-0161406.
PR	09-AUG-1999;	99US-0147493.	PR	25-OCT-1999;	99US-0161406.
PR	09-AUG-1999;	99US-0147935.	PR	26-OCT-1999;	99US-0161359.

Query Match 61.6%; Score 1304; DB 21; Length 402;
 Best Local Similarity 60.3%; Pred. No. 1..e-125;
 Matches 240; Conservative 67; Mismatches 87; Indels 4; Gaps 2;
 QY 6 DATB-EDFUDPWTQVTSSAKGIDYTKLIVRGSSKKIDKELINKRERATQRPHFLR 63

PR . 26-JUL-1999; 99US-0145276.
 PR . 27-JUL-1999; 99US-0145913.
 PR . 27-JUL-1999; 99US-0145918.
 PR . 28-JUL-1999; 99US-0145951.
 PR . 02-OCT-1999; 99US-0146385.
 PR . 02-AUG-1999; 99US-0146388.
 PR . 02-AUG-1999; 99US-0146389.
 PR . 03-AUG-1999; 99US-0147038.
 PR . 04-AUG-1999; 99US-0147204.
 PR . 04-AUG-1999; 99US-0147302.
 PR . 05-AUG-1999; 99US-0147192.
 PR . 05-AUG-1999; 99US-0147260.
 PR . 06-AUG-1999; 99US-0147303.
 PR . 09-AUG-1999; 99US-0147416.
 PR . 09-AUG-1999; 99US-0147493.
 PR . 10-AUG-1999; 99US-0147935.
 PR . 10-AUG-1999; 99US-0148171.
 PR . 11-AUG-1999; 99US-0148319.
 PR . 12-AUG-1999; 99US-0148341.
 PR . 13-AUG-1999; 99US-0148565.
 PR . 13-AUG-1999; 99US-0148684.
 PR . 16-AUG-1999; 99US-0149368.
 PR . 17-AUG-1999; 99US-0149175.
 PR . 18-AUG-1999; 99US-0149426.
 PR . 20-AUG-1999; 99US-0149722.
 PR . 20-AUG-1999; 99US-0149929.
 PR . 23-AUG-1999; 99US-0149902.
 PR . 23-AUG-1999; 99US-0149930.
 PR . 25-AUG-1999; 99US-0150566.
 PR . 26-AUG-1999; 99US-0150884.
 PR . 27-AUG-1999; 99US-0151065.
 PR . 27-AUG-1999; 99US-0151066.
 PR . 29-AUG-1999; 99US-0151080.
 PR . 30-AUG-1999; 99US-0151303.
 PR . 31-AUG-1999; 99US-0151438.
 PR . 01-SEP-1999; 99US-0151930.
 PR . 07-SEP-1999; 99US-0152363.
 PR . 10-SEP-1999; 99US-0153070.
 PR . 13-SEP-1999; 99US-0153758.
 PR . 15-SEP-1999; 99US-0154018.
 PR . 16-SEP-1999; 99US-0154039.
 PR . 20-SEP-1999; 99US-0154779.
 PR . 22-SEP-1999; 99US-0155139.
 PR . 23-SEP-1999; 99US-0155486.
 PR . 24-SEP-1999; 99US-0155659.
 PR . 28-SEP-1999; 99US-0156458.
 PR . 29-SEP-1999; 99US-0156596.
 PR . 04-OCT-1999; 99US-0157117.
 PR . 05-OCT-1999; 99US-0157753.
 PR . 05-OCT-1999; 99US-0157865.
 PR . 07-OCT-1999; 99US-0158029.
 PR . 08-OCT-1999; 99US-0158232.
 PR . 12-OCT-1999; 99US-0158369.
 PR . 13-OCT-1999; 99US-0159293.
 PR . 13-OCT-1999; 99US-0159294.
 PR . 13-OCT-1999; 99US-0159295.
 PR . 14-OCT-1999; 99US-0159329.
 PR . 14-OCT-1999; 99US-0159330.
 PR . 14-OCT-1999; 99US-0159331.
 PR . 14-OCT-1999; 99US-0159637.
 PR . 14-OCT-1999; 99US-0159638.
 PR . 18-OCT-1999; 99US-0159584.
 PR . 21-OCT-1999; 99US-0160741.
 PR . 21-OCT-1999; 99US-0160767.
 PR . 21-OCT-1999; 99US-0160768.
 PR . 21-OCT-1999; 99US-0160814.
 PR . 21-OCT-1999; 99US-0160815.
 PR . 22-OCT-1999; 99US-0160980.
 PR . 22-OCT-1999; 99US-0160981.
 PR . 22-OCT-1999; 99US-0160989.

Query Match₆₁₋₆₄; Score 1304; DB 21; Length 426;
 Best Local Similarity 60.3%; Pred No. 1.2e-125; Mi matches 87; Indels 4; Gaps 2;
 Matches 240; Conservative 67; Mi matches 87; Indels 4; Gaps 2;

QY	6 DATEAB-EDFDPWVQWTSSAKGIDYDYLKIVRGSSSKIDELINERARTQRORPHFLR	63
DB	91 RSVFEEAHDFNBILDAVERGKFKVLYTGRGSSEALHGHJPFEMETKYLQEAFKPVLI	150
QY	124 QMDTDEKWLKDILTDOQAYGDAVENAKDITACGFDTINKTRFSIDLDMGMSSGFYKNVK	183
DB	151 QLTDDERKSIIWNLNSVEESORLARENADIIAGFDVTKFIFSDFDYVG-GAFYKOMV	208
QY	184 IOKHVNENQVKIGFEDSCDGKISPPAOCAPSNSNSPQIFRRTDIOCLICAIQD	243
DB	209 VSGKVUTLNUKAMIGFGSSEGEDPAIKUSPPVQVPSPSPSSFFHLFPCRDNURCLIPAIQD	268
QY	244 DPFYRMTRDVARPGPKALLHSTFPALQAOQTMISASPNSSIFLTDPAQIKTVN	303
DB	269 DPYFRMTRDVARPGKSPALIESTFPALQOGENGKMSASDPNSAIYTVDPSAKDINKIN	328
QY	304 KHFSGGRDTTEFHROFGNCODVDFMMLTFLEDDKLFEQIRKOTYSGAMLGTBLKA	363
DB	329 RYAFSGQQDSLEKHRELGANLEDIVKXLSFFLEDSEBHKKEYGEGRMLTGIVKR	388
QY	364 LIEVLQPLIAEHOARKEVTEIVKERTMTPKLSFDPQ	401
DB	389 LIEVLQPLIEVKEERRARAATVDEWDMAFWAPVPLPSKE	426

RESULT 15
 ID AAB66931 standard; Protein: 424 AA.
 XX AAB66931;
 AC AAB66931;
 DT 12-APR-2001 (first entry)
 XX
 DB Tryptophanyl-tRNA synthetase.
 XX
 KW Tryptophanyl-tRNA synthetase; enzyme.
 OS Candida albicans.
 PN US6174113-B1.
 XX
 PD 16-JAN-2001.
 XX
 PF 16-JUN-1997; 97US-0876885.
 XX
 PR 16-JUN-1997; 97US-0876885.
 XX
 PA (CUB1-) CUBIST PHARM INC.
 XX
 PI Shen X., Houman F.;
 XX
 DR WPI; 2001-201806120.
 DR N-PSDB; AAB55855.

PT New nucleic acids encoding Candida cytoplasmic tryptophanyl-tRNA
 PT (ctrNA) synthetases, useful for producing recombinant ctrNA synthetases
 PT and detecting inhibitor of Candida ctrNA synthetase function

XX

PS Claim 4; Fig 1; 32pp; English.

XX

CC The present sequence is Candida albicans cytoplasmic tryptophanyl-tRNA
 CC (ctrNA) synthetase. ctrNA synthetase is useful for producing recombinant
 CC ctrNA synthetases and detecting inhibitors of ctrNA synthetase.

XX

SQ Sequence 424 AA;

Query Match 57.6%; Score 1218.5; DB 22; Length 424;
 Best Local Similarity 57.1%; Pred. No. 8.4e-17;
 Matches 226; Conservative 71; Mismatches 92; Indels 7; Gaps 3;

QY 8 TEAEEDFVDPWTVQ---TSSRKGDIDKLTVRFGSSKIDKLINIERATGQRPHFLR 63
 Db 13 TESEEQKIPNVEAGAVDGGKSMGIYDKLJSQFGTKHITETTLERPKQVGEERPPFLK 72

Qy 64 RGFIFSHRDMDQVLDAYENKEPFYLTYGRGSSSEAMMVGHLPEITTKWLODVENVPLI 123
 Db 73 RGVFFFSORDLDRILDLVYHEGPFFLYIGRGPSSDSMHLGHMWPFIFPKWLQEVFDVPLVI 132

Qy 124 QMTDDDEKYLWK-DLTQDQAYGDAVENAKDIAACGFINKFTFSQDLYMGNSGFYKVV 182
 Db 133 ELTDDDEKFLPKHQLTDIVKRPAAENAKDIIAVGENTPENTIFSQDLYQYMG--GAFENVV 190

Qy 183 KIQKHTVFNOVKIGKIGFTDSQCGIKSISPPAIOQAPSFSNSPEQIFRDRTDQCLIPCAID 242
 Db 191 RTSRQITSTAKAVFGFTDSQIGKHFASQIQTARPPSFVDVLGLPPKTPPCPCLPCAID 250

Qy 243 QDPYFRMTRDVAAPRIGYPKPALHSHTPPALQGAOTMNSASDPNNSIFLTTDPAOKTKV 302
 Db 251 QDPYFRVCRDVADKLRFTKPAULIHAKEFPALQGASTRMSASDTTISIFMGDTAKOIQKKI 310

Qy 303 NKGHAFSGGRDTIEHDFGMDQDVSPFMVLTTFLEDDDKLQEIRQDTSQAMJGELKK 362
 Db 311 NRYAFSGGRATAEHRBLGGNPEVDVAFQYLSPFSYDKEKLAQEOGYRKGETLISGEMKK 370

Qy 363 ALIEVHQPLIAHQARKEVTDIBIVEKFMTPLRKLSF 398
 Db 371 ECITVLOQEFVSYAQERSKVDDQVSVSKFMKPKHLV 406

Search completed: July 10, 2003, 12:30:12
 Job time : 33.08 secs

